

STIC-Biotech/ChemLib

188683

From: Whiteman, Brian
Sent: Thursday, May 04, 2006 12:56 PM
To: STIC-Biotech/ChemLib
Subject: FW: seq search

10659800

SEQ ID NO 6 against AA and DNA

- 1) issued us patents and published us patent applications
- 2) **commercial databases**

FOR DNA limit to 500 nucleotides or less.

Thank you,

Brian Whiteman
Remsen, 2D14
mail box 2C18
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

CRFE

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

- Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
- Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 5, 2006, 12:28:10 ; Search time 231 Seconds
(without alignments)
1490.467 Million cell updates/sec

Title: US-10-659-800-6
Perfect score: 2594
Sequence: 1 MGDRGSSRRRTGSRPSSHG.....VLMYVHDYVLYNTEAPAAEA 488

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2588	99.8	488	1	DGAT1_HUMAN	O75907 homo sapien
2	2504.5	96.5	491	1	DGAT1_CERAE	O9gm1 ceroplithee
3	2299.5	88.6	500	2	OBBH15_RAT	O8bh15 rattus norv
4	2292.5	88.4	489	2	OBSQBO_BOVIN	O8sqb0 bos taurus
5	2279.5	87.9	489	2	OBNK44_BOVIN	O8mk44 bos taurus
6	2278.5	87.8	498	1	DGAT1_MOUSE	O52a27 mus musculu
7	2278.5	87.8	498	2	O54A6_MOUSE	O54a6 mus musculu
8	2266.5	87.4	489	2	O8MHZ1_PIG	O8mh1 sus scrofa
9	2266.5	87.4	498	1	DGAT1_RAT	O9em3 rattus norv
10	2117	81.6	400	2	O9BRH5_HUMAN	O9br15 homo sapien
11	1686	65.0	499	2	O6P3J0_BRARE	O6p3j0 brachydanid
12	1648.5	63.6	507	2	O6DHG2_BRARE	O6dh2 brachydanid
13	1624	62.6	473	2	O4RLB7_TESTNG	O4rlb7 tetraodon r
14	1608	62.0	447	2	O4RLB8_TESTNG	O4rlb8 tetraodon r
15	1230	47.4	242	2	O9IYB5_RAT	O9iyb5 rattus norv
16	1122.5	43.3	497	2	O60MK6_CAEER	O60mk6 caenorhabd
17	1106	42.6	496	2	O45245_CAEEL	O45245 caenorhabd
18	1106	42.6	498	2	O9NCE1_CAEEL	O9nce1 caenorhabd
15	1102.5	42.5	480	2	O7Q3B6_ANOGA	O7q36 anopheles g
20	1018	39.2	565	2	O960U8_DROME	O960u8 drosophila
21	1018	39.2	615	2	O7KTS2_DROME	O7kts2 drosophila
22	1016	39.2	565	2	O8ST50_DROME	O8st50 drosophila
23	975	37.6	221	2	O4VYU5_BUBBU	O4vyu5 bubalus bu
24	823.5	31.7	498	2	O5GKZ7_SOYBN	O5gkz7 glycine max
25	821	31.6	655	2	O55BH9_DICDI	O55bh9 dicystosell
26	819.5	31.6	511	2	O51ZP3_LOYUA	O51zp3 lotus japon
27	819	31.6	507	2	O5UEW2_BRAUT	O5uew2 eumyrmex a
28	817	31.5	503	2	O4UT38_BRAUT	O4ut38 braasica j
29	800	30.8	406	2	O6DNG3_SOYBN	O6dng3 glycine max
30	797	30.7	532	2	O9SEB9_TOBAC	O9seb9 nicotiana t
31	791.5	30.5	520	2	O9SLD2_ARATH	O9sl2 arabidopsis t

32	788.5	30.4	501	2	O9W4V2_BRANA	O9W4V2_brassica na
33	785.5	30.3	518	2	O8RX96_TROPA	O8RX96_tropaeolum
34	785.5	30.3	534	2	O9FUL6_PEFIFR	O9FUL6_perilla fru
35	784	30.2	503	2	O4U3T9_BRAUT	O4U3T9_brassica ju
36	781.5	30.1	521	2	O67C39_RICCO	O67C39_ricinus com
37	779.5	30.1	503	2	O9XGR5_BRANA	O9XGR5_brassica na
38	774.5	29.9	477	2	O528Z2_ORYSA	O528Z2_oryza sativ
39	767	29.6	538	2	O51396_ORYSA	O51396_oryza sativ
40	759	29.3	532	2	O6ED63_ORYEU	O6ED63_olea europ
41	656.5	25.3	341	2	O9XGV4_BRANA	O9XGV4_brassica na
42	639	24.6	504	2	O688L6_ORYGA	O688L6_oryza sativ
43	585	22.6	508	2	O4X1Y1_ASPEFU	O4X1Y1_aspergillus
44	584	22.5	526	2	O6C9V5_YARLI	O6C9V5_yarrowia li
45	583	22.5	540	2	O7YXK9_TOXGO	O7YXK9_toxoplasma

ALIGNMENTS

RESULT 1

ID	DGAT1_HUMAN	STANDARD	PRT	488 AA.
AC	O75307; Q96B88;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Diacylglycerol O-acyltransferase 1 (EC 2.3.1.20) (Diglyceride acyltransferase) (ACAT-related gene product 1).			
GN	Name=DGAT1; Synonyms=AGRP1, DGAT1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;			
OC	Homo.			
OX	NCBI_Taxid=9606;			
RP	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=98434592; PubMed=9756920; DOI=10.1074/jbc.273.41.26765;			
RA	Oelkner P., Behari A., Cromley D., Billheimer J.T., Sturley S.L.;			
RT	"Characterization of two human genes encoding acyl coenzyme A:cholesterol acyltransferase-related enzymes.";			
RL	J. Biol. Chem. 273:26765-26771(1998).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Yamasaki Y., Watanabe T.K., Tanigami A.;			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
RP	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	TISSUE=Brain, and Skin;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diachenko L.K., Martins A.K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carinini P., Pange C.,			
RA	Rah S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Boes S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumarate P.H.,			
RA	Richards S., Morley K.C., Hale S., Garcia A.W., Gay L.J., Hulys S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J.J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Bucherfeld Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	- FUNCTION: Catalyzes the terminal and only committed step in			
CC	triacylglycerol synthesis by using diacylglycerol and fatty acyl			
CC	CoA as substrates.			
CC	- CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol = CoA +			

```

CC triacylglycerol.
CC -1- PANTHAY: Central role in the metabolism of cellular diacylglycerol
CC lipid.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (By similarity).
CC -1- SIMILARITY: Belongs to the membrane-bound acyltransferase family.
CC Sterol o-acyltransferase subfamily.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL, AF059202; AAC6397.1; -; mRNA.
DR EMBL, AB057815; BAC66170.1; -; mRNA.
DR EMBL, BC015762; AAH15762.1; -; mRNA.
DR EMBL, BC023565; AAH23565.1; -; mRNA.
DR HGNC, HGNC:2843; DGAT1.
DR H-InvDB, HIX0007854; -.
DR Reactome, O75907; -.
DR MIM, 604900; -.
DR GO, GO:0008415; F:acyltransferase activity; TAS.
DR GO, GO:0004144; F:diacylglycerol O-acyltransferase activity; TAS.
DR GO, GO:0006641; P:triacylglycerol metabolism; TAS.
DR InterPro, IPR004299; MBOAT_fam.
DR Pfam, PF03062; MBOAT, 1.
KW Acyltransferase; Endoplasmic reticulum; Transferase; Transmembrane.
FT TRANSMEM 104 124
FT TRANSMEM 130 150
FT TRANSMEM 166 186
FT TRANSMEM 189 209
FT TRANSMEM 282 302
FT TRANSMEM 332 352
FT TRANSMEM 406 426
FT TRANSMEM 428 448
FT TRANSMEM 453 473
FT ACT SITE 415 415
FT CONFLICT 129 129 Y -> H (in Ref. 1).
SQ SEQUENCE 488 AA; 55278 MW; 6574D5DBF15D6171 CRC64;
Query Match 99.8%; Score 2588; DB 1; Length 488;
Best Local Similarity 99.8%; Pred. No. 2.2e-199;
Matches 487; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 421 VPLRMFLMFTGMMAQIPLAMPVGRFPGNYGNAVWLSLIGQPIAVLMYVHDYVLN 480
DB 421 VPLRMFLMFTGMMAQIPLAMPVGRFPGNYGNAVWLSLIGQPIAVLMYVHDYVLN 480
OY 481 YEAPAAEA 488
DB 481 YEAPAAEA 488
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RESULT 2
DQAT1_CERAE STANDARD; PRT; 491 AA.
AC 09GMFL;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Diacylglycerol O-acyltransferase 1 (EC 2.3.1.20) (Diglyceride
DE acyltransferase).
GN Name=DGAT1; Synonyms=DGAT;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Cercopithecoidea; Cercopithecoidea; Cercopithecinae; Cercopithecus.
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Cercopithecoidea; Cercopithecoidea; Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Liver;
RA Joyce C.W., Davis M.A., Anderson R.A., Rudel L.L.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the terminal and only committed step in
CC triacylglycerol synthesis by using diacylglycerol and fatty acyl
CC CoA as substrates.
CC -1- CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol = CoA +
CC triacylglycerol.
CC -1- PATHWAY: Central role in the metabolism of cellular diacylglycerol
CC lipid.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (By similarity).
CC -1- SIMILARITY: Belongs to the membrane-bound acyltransferase family.
CC Sterol o-acyltransferase subfamily.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL, AF236018; AAF98557.1; -; mRNA.
DR InterPro, IPR004299; MBOAT_fam.
KW Acyltransferase; Endoplasmic reticulum; Transferase; Transmembrane.
FT TRANSMEM 107 127
FT TRANSMEM 131 151
FT TRANSMEM 169 189
FT TRANSMEM 192 212
FT TRANSMEM 285 305
FT TRANSMEM 335 355
FT TRANSMEM 404 424
FT TRANSMEM 431 451
FT TRANSMEM 456 476
FT ACT SITE 418 418
SQ SEQUENCE 491 AA; 55644 MW; BFD3683453D588DB CRC64;
Query Match 96.5%; Score 2504.5; DB 1; Length 491;
Best Local Similarity 95.9%; Pred. No. 1.2e-197;
Matches 471; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

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Db	61	GVAASHWELRGRLDOSLPSDSGCFNNNGILMCMVMILISNARLFLEMLIKXGLVDP	120
Qy	118	IQVNSLFLKDPHSWPAECUVIAANPAVAAFQVEKELAVGALTQOGLLHVANLATIC	177
Db	121	IQVNSLFLKDPYSWPAECUVIAANPAVAAFQVEKELAVGALTQOGLLHVANLATIC	180
Qy	178	FPAAVVLVESTTPVGSLLALMAHTLFLKLTSTYRDVNSGCRBARAKAASAGKASSAA	237
Db	181	FPAAVVLVESTTPVGSLLALMAHTLFLKLTSTYRDVNLMCRRBARAKAASAGKASSAA	240
Qy	228	PHVSYSPDNLTRYDLYYFLFAPLTCYELNFPSPRIKRFLLRRIEMLFFTOLOVGLIQ	297
Db	241	PHVSYSPDNLTRYDLYYFLFAPLTCYELNFPSPRIKRFLLRRIEMLFFTOLOVGLIQ	300
Qy	298	QMVVVTIONSMKPFDMODXSRIIERLLKLAVPNHLIWLFFYVLFHSCINAVALMOQPD	357
Db	301	QMVVVTIONSMKPFDMODXSRIIERLLKLAVPNHLIWLFFYVLFHSCINAVALMOQPD	360
Qy	358	REFYRDMNNSSEVTFPMQWNNI.PYHWCICRHFKPMLRBGSSXMMARTGVLASAFHEX	417
Db	361	REFYRDMNNSSEVTFPMQWNNI.PYHWCICRHFKPMLRBGSSXMMARIGVLASAFHEX	420
Qy	418	LVSVLBMFRLMAFTGMAAQITPLAVVGRFQSGNNAAVWMLSLIIGOPALVLMYVHDYX	477
Db	421	LVSVLBMFRLMAFTGMAAQITPLAVVGRFQSGNNAAVWMLSLIIGOPALVLMYVHDYX	480
Qy	478	VLANEAPAAEA 488	
Db	481	VLANEAPVAGA 491	

RESULT 3	Q8BH15_RAT	Q8BH15_RAT	PRELIMINARY;	PRT;	500 AA
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DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, last annotation update)
DE Diacylglycerol acyltransferase.
GN Name=DGAT;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath
OC Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Fischer344/Ducrl, OLETF/Ock, LETO/Ock, Brown-Norway/Crl, and
RC Sprague-Dawley;
RA Harada Y., Matenabe T.K., Tanisami A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062759; BAC43739.1; -, mRNA.
DR EMBL; AB062760; BAC43740.1; -, mRNA.
DR EMBL; AB062761; BAC43741.1; -, mRNA.
DR EMBL; AB062762; BAC43742.1; -, mRNA.
DR EMBL; AB062763; BAC43743.1; -, mRNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPRO04299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KM Acyltransferase; Transferase.
QO SEQUENCE 500 AA; 5708 MW; 1A8592B7762AFBB CRC64;

Query Match	88.6%;	Score 2299.5;	DB 2;	Length 500;
Best Local Similarity	85.9%;	Pred. No. 3.6e-176;		
Matches 427;	Conservative 26;	Mismatches 31;	Indels 13;	Gaps 3

[illegible]

Db	61	TRDROQRVSVDGHEHLELCHR.LQDLSLFSSDSCFSNRYGLIMNCVMLLISNRLFIENLI	120
Qy	110	KYGLIWDPIQVNSLFLKDPHSPWPAECVLIANVFAVAABOVEKRLAVALGLEQAGLLHY	169
Db	121	KYGLIWDPIQVNSLFLKDPHSPWPAECVLIANVFIATVQIEKRLSVALTEQMGLLHY	180
Qy	170	ANLATICFPAAVNLVVESTIPVSGSLAIAHHTILFLKLSRYDVNSWC--RRARAKAAS	227
Db	181	VNLATICFPAAVNLVVESTIPVSGSLPALASYSILFLKLSRYDVNLRCGRVRKAKAAS	240
Qy	228	AGKAKASSAAPHTUSYPDNLTYRDLYYELFAPVLTCEYLNPPSPRIKGFLLRIILEMF	287
Db	241	AGKAKVSGAAQNTVSPDNLTYRDLYYELFAPVLTCEYLNPPSPRIKGFLLRIILEMF	300
Qy	288	FTOLOGLIQOMWPTIONSMMKPFQDMOYSRIERLLKLAVERNHLIWLIFPYLPHSCLN	347
Db	301	FTOLOGLIQOMWPTIONSMMKPFQDMOYSRIERLLKLAVERNHLIWLIFPYLPHSCLN	360
Qy	348	AAVELMQRGDEEFYRDMWNSSVYYFMQNMNIPYKWCIRHXYKMLPRGSSKMARTEY	407
Db	361	AAVELMQRGDEEFYRDMWNSSVYFMQNMNIPYKWCIRHXYKMLPRGSSKMARTEY	420
Qy	408	FLASAFPEHYIVSVLRLMFRLLMAFTQMMAOQLPLAFVGRFPGNGTGNAAVWLSTLIIGORI	467
Db	421	FLASAFPEHYIVSVLRLMFRLLMAFTQMMAOQLPLAFVGRFPGNGTGNAAVWLSTLIIGORV	480
Qy	468	AVLMYVHDYYVLANTYAP	484
Db	481	AVLMYVHDYYVLANTYAP	497

RESULT 4	
Q8SQBO BOVIN	
ID Q8SQBO_BOVIN PRELIMINARY;	PRT; 489 AA

DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
 DE Diacylglycerol acyltransferase 1 (EC 2.3.1.20).
 GN Name=DGAT1;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=1686133; PubMed=11827942; DOI=10.1101/gr.224202;
 RA Grisart B, Coppieiers W, Farnir F, Karim L, Ford C, Berzi P,
 RA Cambiano N, Mni M, Reid S, Simon P, Spelman R, Georges W.,
 RA Snell R.;
 RT "positional candidate cloning of a QTL in dairy cattle: identification
 RT of a missense mutation in the bovine DGAT1 gene with major effect on
 RT milk yield and composition.";
 RL Genome Res. 12:222-231 (2002).
 EMBL: AY065621; AAL43962.1; -, Genomic DNA.
 DR GO: GO:0008415; Fattyacyltransferase activity; IEA.
 DR GO: GO:0004144; Fattyacylglycerol O-acyltransferase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR InterPro: IPR004299; MBOAT_fam.
 DR Pfam: PF03062; MBOAT. 1.
 DR Acyltransferase; Transferase.
 QO SEQUENCE 489 AA; 55601 MW; 4066DBCLB6743253 CRC64;

Query Match	88.4%;	Score 2292.5;	DB 2;	Length 489;
Best Local Similarity	88.0%;	Pred. No. 1.3e-175;		
Matches 434;	Conservative 15;	Mismatches 31;	Indels 13;	Gaps 3

[illegible]

```
Db 55 DVGSGHMDLRCHRLQDSLFSSDSGFSNVRGILNMCVWMLLSNARLFLENLIKYGILVDP 114
118 IQVNSLFKDPHSPAPCLVIAANVFAVAFOVEKRLAVGALTEOAGLLHVAVALATTLC 177
115 IQVNSLFKDPYSWPALCLVIAVIFAFAAFQVEKRLAVGALTEOAGLLHGVNLTATLC 174
178 FPAVAVLLVESITTPVGSLLAAMAHTILFLKLFSTRDVNSWCR-----ARAKASAGKAS 233
175 FPAVAVFLBESITTPVGSVLAAMVITILFLKLFSTRDVNLMCHERBAGAKAKAALAGKAN 234
234 SAAPHTVSYDPNLTYYRDLYYFLFAPTLCYELNPPSPRIKRLRLRILEMLEFTQLOV 293
235 GGAQRITVSYDPNLTYYRDLYYFLFAPTLCYELNPPSPRIKRLRLRILEMLEFTQLOV 294
Db 294 GLIQOMVPTIIONSKMPKMDYSRIERLKLAVPNHLIWLIFPYWLFHSCUNAVALEM 353
295 GLIQOMVPAIIONSKMPKMDYSRIERLKLAVPNHLIWLIFPYWLFHSCUNAVALEM 354
Qy 354 QFGDREFYRDWNNSESVTYFMQNNNI PVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAF 413
355 QFGDREFYRDWNNSESVTYFMQNNNI PVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAF 414
Db 414 FHEYLVSPLMFLMAFTGMAAQIPLAMFVGRFFQGNVGNAAVWLSLITGPIAVLMYV 473
415 FHEYLVSPLMFLMAFTGMAAQIPLAMFVGRFFQGNVGNAAVWLSLITGPIAVLMYV 474
Qy 474 HDYVLYNTEAPAA 486
475 HDYVLYNTEAPAA 487
Db
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RESULT 5

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Q8MK44_BOVIN PRET; 489 AA.
ID Q8MK44_BOVIN PRELIMINARY; PRT; 489 AA.
AC Q8MK44;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Acyl-CoA:1,2-diacylglycerol O-transferase (EC 2.3.1.20).
GN Name=Dgat1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22103627; PubMed=12077321; DOI=10.1073/pnas.142293799;
RA Witter A., Kramer W., Werner F.A.O., Kollers S., Kata S.,
RA Dusterewitz G., Bultkamp J., Womack J.E., Thaller G., Fries R.;
RT "Association of a lysine-232[Cj81134]alanine polymorphism in a bovine
RT gene encoding acyl-CoA:diacylglycerol acyltransferase (DGAT1) with
RT variation at a quantitative trait locus for milk fat content.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9300-9305(2002).
DR EMBL: AJ18490; CAC86391.1; -; Genomic DNA.
DR GO: GO:0008415; F:acyltransferase activity; IEA.
DR GO: GO:0004144; F:diacylglycerol O-acyltransferase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR004299; MBOAT_fam.
DR Pfam: PF03062; MBOAT_1.
KW Acyltransferase; Transferase.
SQ SEQUENCE 489 AA; 55445 MW; 5C09258DDA027053 CRC64;
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Query Match 87.9%; Score 2279.5; DB 2; Length 489;
Beat Local Similarity 87.6%; Pred. No. 1.4e-174;
Matches 432; Conservative 15; Mismatches 33; Indels 13; Gaps 3;
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Qy 1 MGDR---SSRRRRGRSPSSHGSGGPAAREEVDAAGPVGGAAGAPAPAPKMGDA 57
1 MGDRGAGGSRRRRGRSPSIGSGGPAAREEV-----DVGGAGDPVARDTDDGDV 54
Qy 58 GVSGSHWEIRCHRLQDSLFSSDSGFSNVRGILNMCVWMLLSNARLFLENLIKYGILVDP 117
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Db 55 DVGSGHMDLRCHRLQDSLFSSDSGFSNVRGILNMCVWMLLSNARLFLENLIKYGILVDP 114
118 IQVNSLFKDPHSPAPCLVIAANVFAVAFOVEKRLAVGALTEOAGLLHVAVALATTLC 177
115 IQVNSLFKDPYSWPALCLVIAVIFAFAAFQVEKRLAVGALTEOAGLLHGVNLTATLC 174
178 FPAVAVLLVESITTPVGSLLAAMAHTILFLKLFSTRDVNSWCR-----ARAKASAGKAS 233
175 FPAVAVFLBESITTPVGSVLAAMVITILFLKLFSTRDVNLMCHERBAGAKAKAALAGKAN 234
234 SAAPHTVSYDPNLTYYRDLYYFLFAPTLCYELNPPSPRIKRLRLRILEMLEFTQLOV 293
235 GGAQRITVSYDPNLTYYRDLYYFLFAPTLCYELNPPSPRIKRLRLRILEMLEFTQLOV 294
Db 294 GLIQOMVPTIIONSKMPKMDYSRIERLKLAVPNHLIWLIFPYWLFHSCUNAVALEM 353
295 GLIQOMVPAIIONSKMPKMDYSRIERLKLAVPNHLIWLIFPYWLFHSCUNAVALEM 354
Qy 354 QFGDREFYRDWNNSESVTYFMQNNNI PVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAF 413
355 QFGDREFYRDWNNSESVTYFMQNNNI PVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAF 414
Db 414 FHEYLVSPLMFLMAFTGMAAQIPLAMFVGRFFQGNVGNAAVWLSLITGPIAVLMYV 473
415 FHEYLVSPLMFLMAFTGMAAQIPLAMFVGRFFQGNVGNAAVWLSLITGPIAVLMYV 474
Qy 474 HDYVLYNTEAPAA 486
475 HDYVLYNTEAPAA 487
Db
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RESULT 6

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DGAT1_MOUSE STANDARD; PRT; 498 AA.
ID DGAT1_MOUSE STANDARD; PRT; 498 AA.
AC Q922A7; Q9D705;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Diacylglycerol O-acyltransferase 1 (EC 2.3.1.20) (Diacylceride
DE acyltransferase).
GN Name=Dgat1; Synonyms=Dgat;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6;
RX MEDLINE=99007259; PubMed=9789033; DOI=10.1073/pnas.95.22.13018;
RA Cases S., Smith S.J., Zheng Y.-W., Myers H.M., Lear S.R., Sande E.,
RA Novak S., Collins C., Welch C.B., Lusb A.V., Erickson S.K.,
RA Farese R.V., Jr.;
RT "Identification of a gene encoding an acyl CoA:diacylglycerol
RT acyltransferase, a key enzyme in triacylglycerol synthesis";
RL Proc. Natl. Acad. Sci. U.S.A. 95:13018-13023(1998).
```

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]

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RP STRAIN=C57BL/6; TISSUE=Tongue;
RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Oeato N., Saito R., Suzuki H., Yamazaki I.,
RA Yagi K., Tomaru Y., Haegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schiml L.M., Kanapin A., Matsuda H., Batilov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalia B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giesel C., Godzik A., Gough J.,
RA Grimmond S., Guertlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongnara A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
```

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempé C.A., Seton M., Shimada K.,
 RA Sulana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki N.,
 RA Hirazane-Kihikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hahizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 (3)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX MEDLINE:22388257; PubMed:12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappenbrock M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Parnce C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollahy S.J.,
 RA Bobak S.A., McBreen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyn S.W.,
 RA Villalón D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs S.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakester R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerber A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC - FUNCTION: Catalyzes the terminal and only committed step in
 CC triacylglycerol synthesis by using diacylglycerol and fatty acyl
 CC CoA as substrates.
 CC - CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol = CoA +
 CC triacylglycerol.
 CC - PATHWAY: Central role in the metabolism of cellular diacylglycerol
 CC lipid.
 CC - SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum.
 CC - SIMILARITY: Belongs to the membrane-bound acyltransferase family.
 CC Sterol o-acyltransferase subfamily.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL: AF078752; AAC72917.1; -; mRNA.
 DR EMBL: AK008995; -; NOT_ANNOTATED_CDS; mRNA.
 DR EMBL: BC003717; AA003717.1; -; mRNA.
 DR Ensemble: ENSMUSG000002255; Mus musculus.
 DR MGI: MGI:133825; Dgat1.
 DR GO: GO:0016021; C:Integral to membrane; TAS.
 DR GO: GO:0005624; C:membrane fraction; IDA.
 DR GO: GO:0003846; F:2-acylglycerol O-acyltransferase activity; IDA.
 DR InterPro: IPR004299; MBOAT_fam.
 DR Pfam: PF03062; MBOAT, 1.
 KW Acyltransferase; Endoplasmic reticulum; Transferase; Transmembrane.
 FT TRANSMEM 133 133 potential.
 FT TRANSMEM 139 159 potential.
 FT TRANSMEM 175 195 potential.
 FT TRANSMEM 198 218 potential.

FT TRANSMEM 293 313 potential.
 FT TRANSMEM 343 363 potential.
 FT TRANSMEM 417 437 potential.
 FT TRANSMEM 439 459 potential.
 FT TRANSMEM 464 484 potential.
 FT ACT SITE 426 426 potential.
 SQ SEQUENCE 498 AA; 56790 MW; E7BDD6DDCF1EC2B CRC64;
 Query Match 87.8%; Score 2278.5; DB 1; Length 498;
 Best local Similarity 85.1%; Pred. No. 1,76-174;
 Matches 421; Conservative 29; Mismatches 34; Indels 11; Gaps 3;
 QY 1 MGDRL--GSSRRRTGSRPSRHGGGPPAAAEVRDPAAGAPVGAADAPAPAP----- 51
 DB 1 MGDRLGAGSSRRRTGSRPSRHGGGPPAAAEVRDPAAGAPVGAADAPAPAPAPAPAPAPAP 60
 QY 52 MKDGDAGVSGHWEIRCHRLQDSLFSSDSGSESNYRGLNWCVMVLTLSNARLFLENLIRY 111
 DB 61 DDKGRSTVGDGYMDLRCHRLQDSLFSSDSGFSPNYRGLNWCVMVLTLSNARLFLENLIRY 120
 QY 112 GLVDPIDVSLFLDPSHWPAPCVIANFAVAFOVEKRLAVGALTEQGLLVAN 171
 DB 121 GLVDPIDVSLFLDPSHWPAPCVIANFAVAFOVEKRLAVGALTEQGLLVAN 180
 QY 172 LATILCFPAAVLVLESITPVGSLTAMHTILFLKESYRDVNSWC--RRARAAASAG 229
 DB 181 LATILCFPAAVLVLESITPVGSLTAMHTILFLKESYRDVNSWC--RRARAAASAG 240
 QY 230 KKAASAAAPHTVSYDNLITRDLYFLPAVLYCELNFPSPRIKRRFLIRILEMLFTT 289
 DB 241 KKVSGAAAOAAVSPDNLITRDLYFLPAVLYCELNFPSPRIKRRFLIRILEMLFTT 300
 QY 290 QLVGLIQOMVPTIQNSMKPKMDYSRIERLKLAVPNLILVLFYMFHSCLVAN 349
 DB 301 QLVGLIQOMVPTIQNSMKPKMDYSRIERLKLAVPNLILVLFYMFHSCLVAN 360
 QY 350 AELMFGDREFPRDMWNSVYTFWQNNIPVHKVCIRHFYKPMLRGSSKMAATGVFL 409
 DB 361 AELMFGDREFPRDMWNSVYTFWQNNIPVHKVCIRHFYKPMLRGSSKMAATGVFL 420
 QY 410 ASAFHEILVSVPLFMFLMAFTGMAOPIPLAMVGRFFQNGYGAUAVLSLITGPIAV 469
 DB 421 TSAPFHEILVSVPLFMFLMAFTGMAOPIPLAMVGRFFQNGYGAUAVVLTILIGPVAV 480
 QY 470 LMYVDYVLYNVEAP 484
 DB 481 LMYVDYVLYNVEAP 495
 Db
 RESULT 7
 ID Q54AA6_MOUSE PRELIMINARY; PRT; 498 AA.
 AC Q54AA6;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Diacylglycerol acyltransferase.
 GN Name=Dgat1; Synonyms=Dgat;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamasaki Y., Watanabe T.K., Tanigami A.;
 RT "Mus musculus diacylglycerol acyltransferase (Dgat) mRNA, complete
 RT cds";
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB057816; BAC66171.1; -; mRNA.
 DR MGI: MGI:133825; Dgat1.
 DR GO: GO:0016021; C:Integral to membrane; TAS.
 DR GO: GO:0005624; C:membrane fraction; IDA.

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Brown Norway; TISSUE=Brain;
 RA Zhang Y., Yang Q., Baese P., Rice P.;
 RT "Cloning of a rat novel gene encoding an acyl CoA:diacylglycerol
 acyltransferase, a key enzyme in triacylglycerol synthesis."
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Catalyzes the terminal and only committed step in
 triacylglycerol synthesis by using diacylglycerol and fatty acyl
 CoA as substrates.
 CC -1- CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol = CoA +
 triacylglycerol.
 CC -1- PATHWAY: Central role in the metabolism of cellular diacylglycerol
 lipids.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 reticulum (By similarity).
 CC -1- SIMILARITY: Belongs to the membrane-bound acyltransferase family.
 CC Sterol O-acyltransferase subfamily.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 CC EMBL: AF296131; AAG10084.1; -; mRNA.
 DR Ensembl: ENSRNOC0000028711; Rattus norvegicus.
 DR RGD: 628673; Dgat1.
 DR InterPro: IPR004299; MBOAT_fam.
 DR Pfam: PF03062; MBOAT_1.
 KW Acyltransferase; Endoplasmic reticulum; Transferase; Transmembrane.
 FT TRANSMEM 113 133 Potential.
 FT TRANSMEM 139 159 Potential.
 FT TRANSMEM 175 195 Potential.
 FT TRANSMEM 198 218 Potential.
 FT TRANSMEM 293 313 Potential.
 FT TRANSMEM 343 363 Potential.
 FT TRANSMEM 417 437 Potential.
 FT TRANSMEM 439 459 Potential.
 FT TRANSMEM 464 484 Potential.
 FT ACT SITE 426 426 Potential.
 SQ SEQUENCE 498 AA; 56870 MW; 5B24DD4AEB87CB4D CRC64;

Query Match 87.4%; Score 2266.5; DB 1; Length 498;
 Best Local Similarity 85.1%; Pred. No. 1.6e-173;
 Matches 421; Conservative 28; Mismatches 35; Indels 11; Gaps 3;

QY 1 MGBR---GSSRRRTGSRPSSHGCGGPAABEEVDDAAGAPVGAAGAPAPAP----- 51
 DB 1 MGBRGGAGSSRRRRRGSRVSVGGSGPKVEDEVEEAASVPLDAGADAPAPAPAHTR 60
 QY 52 NKDDGAGVSGHWEIQRHLDOSLSSDSGFSNNGIINWCVMLILSNARLFENLKY 111
 DB 61 DKDRTSVGGDGWEIQRHLDOSLSSDSGFSNNGIINWCVMLILSNARLFENLKY 120
 QY 112 GILVDPPIQVSLFLKDPSPWPAPCLVIANVFAVAFOVEKRLAVGALTEOAGLLHYAN 171
 DB 121 GILVDPPIQVSLFLKDPSPWPAPCLVIANSFIYATFQIEKRLSGALTEOAGLLHYAN 180
 QY 172 LATILCPFAAVVLLVESTTPVGSLLAAMHTILFKLPSYRDVSWC--RRAPATAASAG 229
 DB 181 LATILCPFAAVVLLVESTTPVGSLLAAMHTILFKLPSYRDVSWC--RRAPATAASAG 240
 QY 230 KKASAAAPHTVSPDNLTYRDLYFLAPTLCEVLPNPRSPRIKRLFLRIEMLEFFT 289
 DB 241 KKVSGAAQNTVSPDNLTYRDLYFLAPTLCEVLPNPRSPRIKRLFLRIEMLEFFT 300
 QY 290 QLVGGLIOQNVVPTIQQNSMKPFKMDYSGRIERLKLAVPNHLIWLIFPYMLFHSCLNAV 349
 DB 301 QLVGGLIOQNVVPTIQQNSMKPFKMDYSGRIERLKLAVPNHLIWLIFPYMLFHSCLNAV 360
 QY 350 AELMQFGDREFRDWMSSESTVFQWQNNIPVHKCIRHFYKPMIRGSSKMAATGVPL 409
 DB 361 AELLQFGDREFRDWMSSESTVFQWQNNIPVHKCIRHFYKPMIRGSSKMAATGVFW 420

QY 410 ASAFPHETLVSVPLBMPRLMAFTGMAOIPLAMPVGRFPQNGYXGNAAVLSTLIGOPNAV 469
 DB 421 ASAFPHETLVSVPLBMPRLMAFTGMAOIPLAMPVGRFPQNGYXGNAAVLSTLIGOPNAV 480
 QY 470 LMTYVDHYVLYNLEAP 484
 DB 481 LMTYVDHYVLYNLEAP 495

RESULT 10
 Q9BRH5 HUMAN
 ID Q9BRH5 HUMAN PRELIMINARY; PRT; 400 AA.
 AC Q9BRH5;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Dgat1 protein (Fragment).
 GN Name=Dgat1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovary;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnae.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S., Krzywinski M.I., Skalski U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences".
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovary;
 RA Strausberg R.;
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC006263; AA06263.4; -; mRNA.
 DR GO: GO:0005489; F:electron transporter activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR004299; MBOAT_fam.
 DR Pfam: PF03062; MBOAT_1.
 FT NON_TER 1
 SQ SEQUENCE 400 AA; 46347 MW; 493AA57816568B63 CRC64;

Query Match 81.6%; Score 2117; DB 2; Length 400;
 Best Local Similarity 99.8%; Pred. No. 1.3e-161;
 Matches 399; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 89 LNMCVMLILSNARLFENLKYGILVDPPIQVSLFLKDPSPWPAPCLVIANVFAVAAP 148
 DB 1 LNMCVMLILSNARLFENLKYGILVDPPIQVSLFLKDPSPWPAPCLVIANVFAVAAP 60
 QY 149 QVEKRLAVGALTEOAGLLHYANLATIICFPAAVVLLVESTTPVGSLLAAMHTILFKL 208
 DB 61 QVEKRLAVGALTEOAGLLHYANLATIICFPAAVVLLVESTTPVGSLLAAMHTILFKL 120

QY 209 FSYRDVSWCRBARAKASAGKSSAAAPHTVSVDNLTYRDLYFLFAPLTCYELNFP 268
 DB 121 FSYRDVSWCRBARAKASAGKSSAAAPHTVSVDNLTYRDLYFLFAPLTCYELNFP 180
 QY 269 RSPRIKRFLLRILEMFLPTQLQVGLIQOMWVPTIOMSKRPFKMDYSRIIRLLKLAIV 328
 DB 181 RSPRIKRFLLRILEMFLPTQLQVGLIQOMWVPTIOMSKRPFKMDYSRIIRLLKLAIV 240
 QY 329 PNLILWILFFWYLFHSCINAAVAELMQDREDFRDMWNSSESTYTWOMWNIPIVHKWCI 388
 DB 241 PNLILWILFFWYLFHSCINAAVAELMQDREDFRDMWNSSESTYTWOMWNIPIVHKWCI 300
 QY 389 FYKMLRGRSSKMMARVGPFLASAFHELYSVPLRMFRLMAFTGMAQIPLAMFVGRFF 448
 DB 301 FYKMLRGRSSKMMARVGPFLASAFHELYSVPLRMFRLMAFTGMAQIPLAMFVGRFF 360
 QY 449 QGNYGNAAVMLSLIIGDPIAVLMVVDYVLYNTEAPAAEA 488
 DB 361 QGNYGNAAVMLSLIIGDPIAVLMVVDYVLYNTEAPAAEA 400
 RESULT 11
 Q6P3J0 BRABE PRELIMINARY; PRT; 499 AA.
 AC Q6P3J0
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE Hypothetical protein zgc:77691.
 GN ORFNames=zgc:77691;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_taxonomy=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Hopkin L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshlyuk S., Abramson R.D., Mullany S.J.,
 RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dixon M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole;
 RA Strausberg R.L.
 RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC063970; AAH63970.1; -; mRNA.
 DR ZFIN; ZDB-GENE-030131-4600; zgc:77691.
 DR InterPro; IPR004299; MBOAT_fam.
 DR Pfam; PF03062; MBOAT_1.
 KM Hypothetical protein
 SQ SEQUENCE 499 AA; 57151 MW; 3B3E3DA7685AEDF4 CR664;

Matches 323; Conservative 58; Mismatches 97; Indels 28; Gaps 8;
 QY 1 MGDR---GSSRRRTGSRPSSHGCGPAAAEVRYDAAGDVGAGDAPAPAPNNK-DGD 56
 DB 1 MGDRNEKGSAGHRRRTT-----SGEAAVYQARGGAEE--LSQVKEKEQKXENA 51
 QY 57 AGVSGHME-----LRCHRLQDSLFSDDSGFSNYRGLNMCVMLISNARPLENTIKY 111
 DB 52 AGRQKNSDAGEDPFSCHKQESLSSASGFSNYRGLNMCVMLVLSNARPLENTIKY 111
 QY 112 GILVDPQLQVSLFLKDPHSPAPCLVLAANYEVAQAQVEKRLAVGLTEQAGLLIVAN 171
 DB 112 GVLVDPLQIISLFXKDCPSMPALCLITVNFVMAALYTERKLSVGTISERTGSLICIN 171
 QY 172 LATLCPFAAVLLVVESTITPVSLLAAMHTILFLKFSYRDVSWCRBAR-ARASAGK 230
 DB 172 LSAULFPVAGVLSLSTVTPGVSMALSTICVLKLYSTYDVNKKREGQAARTLSR 231
 QY 231 -----KSSAAAPHTVSVDNLTYRDLYFLFAPLTCYELNFPSPRIKRFLLRL 282
 DB 232 SHSCPSYKANGTAGYTHVTYPGNLTHRDYFYFAFAPLTCYELNFPSPRIKRFLLRL 291
 QY 283 LEMLFPTQLQVGLIQOMWVPTIOMSKRPFKMDYSRIIRLLKLAIVNHLILFFWYLF 342
 DB 292 LEMLFMLQWGLIQOMWVPTIOMSKRPFKMDYSRIIRLLKLAIVNHLILFFWYLF 351
 QY 343 HSCINAAVAELMQDREDFRDMWNSSESTYTWOMWNIPIVHKWCIHFYKPMRLRSGSKM 402
 DB 352 HSNMFAVEIQLQDREDFRDMWNSSESTYTWOMWNIPIVHKWCIHFYKPMRLRSGSKM 411
 QY 403 ARTGVFLASAFHELYSVPLRMFRLMAFTGMAQIPLAMFVGRFFQGNNGNAAVMLSLI 462
 DB 412 AQIAVFFLSAFHELYSVPLRMFRLMAFTGMAQIPLAMFVGRFFQGNNGNAAVMLSLI 471
 QY 463 IGPPIAVLMVVDYVLYNTEAPAAEA 488
 DB 472 IGPPIAVLMVVDYVLYNTEAPAAEA 496
 RESULT 12
 Q6DHG2 BRABE PRELIMINARY; PRT; 507 AA.
 AC Q6DHG2
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DE Zgc:92327.
 GN ORFNames=zgc:92327;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_taxonomy=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Hopkin L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshlyuk S., Abramson R.D., Mullany S.J.,
 RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dixon M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,

Query Match 65.0%; Score 1686; DB 2; Length 499;
 Best Local Similarity 63.8%; Pred. No. 7,4e-127;

RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Whole;

RA Strusberg R.;

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC076012; AAH76012.1; -; mRNA.

DR ZFIN: ZDB-GENE-040718-158; zgc:92327.

DR InterPro: IPR004289; MBOAT_fam.

DR Pfam: PF03062; MBOAT; 1.

SQ SEQUENCE 507 AA; 58757 MW; AE481F09E067FA9 CRC64;

Query Match 63.6%; Score 1648.5; DB 2; Length 507;

Best Local Similarity 64.7%; Pred. No. 7.8e-124;

Matches 306; Conservative 58; Mismatches 72; Indels 37; Gaps 4;

41 GAAGAPAPAPKDDAGVSGHW-----ELRCRLQDLP 77

32 GAAATPAA-----ADSGKSGHKARSLAKNLQNEKRCDRYDRKSGKLGESMIS 85

78 SDGFSNTRGILNMCVMIISNARILENLIKYGILVDPQIVSILFKDPSWPAICLV 137

86 SASSFKNYRGILNMCVMIISNARILENLIKYGILVDPQIVSILFKDPSWPAICLV 145

138 IAAAPFAVAPOVEKRLANGALTEQAGILLAHANLATICFPAAVVLVESTTPGSLA 197

146 IVCNPFILVALYTERLTLANGSISEKGLIYIFNLTILCFPMVVVLKLPSTIPPGAPA 205

198 IMAHTILFLKFSYRDVNSWCR-RARAKASAGKASAAAPHT-----VSPDNLTY 249

206 LGIYITILFLKXSYDVNKKCKERTQAKRSLSRLSCSPSPSTSSMSQSYSTGNLST 265

250 RDLYYFLPAPTLCYELNPPSPRIKRFILRLILEMLFPTQLQVGLIQGMVPTIQNSMK 309

266 RDIYFVFPAPTLCYELNPPSPRIKRFILRLILEMLFPTQLQVGLIQGMVPTIQNSMK 325

310 PKDMDSRIIERLKLAVPNHLIWLIFPYMLFHSCLNAVALMORGDREPRDMWNS 369

326 PLOEDYTRMTERLKLAVPNHLIWLIFPYMLFHSCLNAVALMORGDREPRDMWNS 385

370 VTYFMQNNNIPVHKMCIHFYKPMRLRGSSKMMARTGVFLASAFHEYLVSPLMFRIM 429

386 IITYFMQNNNIPVHKMCIHFYKPMRLRGSSKMMARTGVFLASAFHEYLVSPLMFRIM 445

430 AFTGMAQIPLAMFVGRFGQNGYNAAVWLSLIIIGQPIAVLMYVDYVLYN 482

446 AFMGMAQIPLAMFVGRFGQNGYNAAVWLSLIIIGQPIAVLMYVDYVLYN 498

RESULT 13

Q4RLB7.TEING PRELIMINARY; PRT; 473 AA.

DT 13-SEP-2005 (TREMBLrel. 31, Created)

DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)

DE Chromosome 21 SCAF15022, whole genome shotgun sequence.

DE (Fragment).

GN ORFNames=GSTENG00032560001;

OS Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Acanthopterygii; Acanthopterygii; Perciformes; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

OC NCBI_TaxID=99883;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouteau L., Fischer C., Ozout-Costaz C., Bernot A.,

RA Niclaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

RA Anthouard V., Jubin C., Castellani V., Katin M., Vachet B.,

RA Bismont C., Skalli Z., Catalicio L., Boulain J., De Berardinis V.,

RA Cruaud C., Duprat S., Brotier P., Coutanceau J.P., Gouzy J.,

RA Parra G., Lardier G., Chappe C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Volt J.N., Guilo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,

RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals

the early vertebrate proto-karyotype";

RL Nature 431:946-957 (2004).

RP NUCLEOTIDE SEQUENCE.

RG Genoscope; Whitehead Institute Centre for Genome Research;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

preliminary data.

DR EMBL: CAAB01015022; CAG10815.1; -; Genomic DNA.

FT NON TER 1 473

SQ SEQUENCE 473 AA; 55366 MW; 0CE0F20F5093342 CRC64;

Query Match 62.6%; Score 1624; DB 2; Length 473;

Best Local Similarity 63.8%; Pred. No. 6.7e-122;

Matches 301; Conservative 51; Mismatches 62; Indels 58; Gaps 3;

68 CHRLQDLSFSDGFSNTRGILNMCVMI-----ILSNA 101

1 CHVLQESLSSASGNSYRGILNMCVMIIFGSGFIASGALGHQGLLIDAFPMKAVLSNA 60

102 RLFLNLIKYGILVDPQIVSILFKDPSWPAICLVIANVAVAPVEKRLANGALTE 161

61 RLFLNLIKYGILVDPQIVSILFKDPSWPAICLVIANVAVAPVEKRLANGALTE 120

162 QAGLLAHVANLATICFPAAVVLVESTTPGSLALMAHTILFLKFSYRDVNSWCRRA 221

121 TTRGILHLFNLASLILFPSATVLTVPMTIPGSGVSLGITYLFLKXSYDNTNRCRI 180

222 R-ARAKASAGKASAAAPHTVSYDNLTYRDLTYFLPAPTLCYELNPPSPRIKRFILR 280

181 ROAKAKRLTRYSCEGFHLLLEPRVENSDMYPTFPAPTLCYQLNPPSPRIKRFILR 240

281 RLTEM-----LAFTQLQVGLIQGMVPTIQNSMK 309

241 RLFEVIRGNAYAAKYSITLPNRRITLTVLHFCILQLFFMQLVGLIQGMVPTIQNSMK 300

310 PKDMDSRIIERLKLAVPNHLIWLIFPYMLFHSCLNAVALMORGDREPRDMWNS 369

301 PLOEDYTRMTERLKLAVPNHLIWLIFPYMLFHSCLNAVALMORGDREPRDMWNS 360

370 VTYFMQNNNIPVHKMCIHFYKPMRLRGSSKMMARTGVFLASAFHEYLVSPLMFRIM 429

361 VTYFMQNNNIPVHKMCIHFYKPMRLRGSSKMMARTGVFLASAFHEYLVSPLMFRIM 420

430 AFTGMAQIPLAMFVGRFGQNGYNAAVWLSLIIIGQPIAVLMYVDYVLYN 481

421 AFMGMAQIPLAMFVGRFGQNGYNAAVWLSLIIIGQPIAVLMYVDYVLYN 472

RESULT 14

Q4RI38.TEING PRELIMINARY; PRT; 447 AA.

DT 13-SEP-2005 (TREMBLrel. 31, Created)

DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)

DE Chromosome 8 SCA115044, whole genome shotgun sequence.

DE (Fragment).

GN ORFNames=GSTENG00034052001;

OS Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphae; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OK NCBI_taxid=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomas N.,
 Maucell E., Bonneau L., Flecher C., Ozouf-Costaz C., Bernot A.,
 Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 Daubivaud V., Jubin C., Castel V., Katinka M., Castellano S.,
 Blemont C., Skallil Z., Caticolico L., Poulin J., De Berardinis V.,
 Crnaud C., Duprat S., Broctier P., Couanceau J.P., Gouzy J.,
 Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 Kellis M., Volff J.N., Gligo R., Zody M.C., Mesirov J.,
 Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 Landet V., Schachter V., Queller F., Sautin W., Scarpelli C.,
 Winkler P., Lander E.S., Weissbach J., Roest Croillais H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.",
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; CAAB01015044; CAG11944.1; -; Genomic_DNA.
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 447 AA; 52106 MW; E335A2785B3CDBFA CRC64;
 Query Match 62.0%; Score 1608; DB 2; Length 447;
 Best Local Similarity 66.4%; Pred. No. 1.2e-120;
 Matches 296; Conservative 52; Mismatches 70; Indels 28; Gaps 4;
 QY 68 CHR.LDDSLFSSDSGSFNSVNGILNMCVMTLISNARLFLENLTKYGLVDPIDVNSFLKD 127
 DB 1 CHR.MDLSLSASGSKRGILNMCVMTLVLSNAHFLLENLTKYGLVDPIDVNSFLND 60
 QY 128 PHSWPAFCVLIAVYFAVAFAOVERKRLAVGALTQAGLLAHVANIATLTCPPAAVVLVE 187
 DB 61 PYSWPAACIVIAVYFAVVALYTERQLSKGSFSEKGLIHCNMAVLTTPPAAVVLLLP 120
 QY 168 SITP-----VGSLLAAMAHTLLPLKFSYRDVNSWCCR-ARAKAASGKXASAAAH 239
 DB 121 SVTPSVQSSGVGAASALSITVTLPLKLYSYKDVNLWCRESLTIKVKLSRLSLCPSOQH 180
 QY 240 -----TVSYPDNLTYRDLYFLFAPTLCYELNFPSPRIRKFLRLILEMLFTLOLV 293
 DB 181 PSGGCKKSYSPGNLTIRDMYTFVFAPTLCYELNFPSPRIRKFLRLILEMLFTLOLV 240
 QY 294 GLIQMNVPTIONSMPKMDYSRIIERLLKLAVPNHLIWLIFPYWLFHSCINAVAEIM 353
 DB 241 ALTQGMVPIIRSSMKPLEDMDSRAERLLRLAVPNHLLMFMFYWPHSSMNFABEL 300
 QY 354 QPDGEFPRDMWNSSVTYFPMQNNIPVHKMCIRHFYKMLRSGSKXMAATGCVPLASAF 413
 DB 301 RFGDRQFNDWMSSEVTVYFMQNNIPVHKMCIRHFYKMLRSGSKXMAATGCVPLASAF 360
 QY 414 PHBYLVSVPLRMFLMAFTGMAA-----QIPLAFVGRFQNGYGNAAVWL 459
 DB 361 PHBYLVSVPLRMFLMAFTGMAA-----QIPLAFVGRFQNGYGNAAVWL 420
 QY 460 SLIIQPIAVLMTYVDYVLYVLAEP 485
 DB 421 SLIIQPIAVLMTYVDYVLYVLAEP 446

AC Q91YB5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Diacylglycerol acyltransferase I (EC 2.3.1.20) (Fragment).
 GN Name=dgat1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OK NCBI_taxid=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Miscar; TISSUE=Liver;
 RA Waterman I.J., Zammit V.A., Price N.T.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ345014; CAC69884.1; -; mRNA.
 DR GO; GO:0008415; F:acyltransferase activity; IEA.
 DR GO; GO:0004144; F:diacylglycerol O-acyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro: IPR004299; MBOAT_fam.
 DR Pfam: PF03062; MBOAT_1.
 KW Acyltransferase; Transferase.
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 242 AA; 29014 MW; E12F6ADA30988542 CRC64;
 Query Match 47.4%; Score 1230; DB 2; Length 242;
 Best Local Similarity 92.5%; Pred. No. 1.4e-90;
 Matches 221; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
 QY 219 RRAKAKASAGKKAASAAAPHTVSYPDNLTYRDLYFLFAPTLCYELNFPSPRIRKFL 278
 DB 4 RRVAKAKASAGKKSAGAAQNTVSYPDNLTYRDLYFLFAPTLCYELNFPSPRIRKFL 63
 QY 279 LRRILEMLFTLOLVGLIQMNVPTIONSMPKMDYSRIIERLLKLAVPNHLIWLIF 338
 DB 64 LRRVLEMLFTLOLVGLIQMNVPTIONSMPKMDYSRIIERLLKLAVPNHLIWLIF 123
 QY 339 YWLFHSCINAVAEIMQPDGEFPRDMWNSSVTYFPMQNNIPVHKMCIRHFYKMLRSGS 398
 DB 124 YWLFHSCINAVAEIMQPDGEFPRDMWNSSVTYFPMQNNIPVHKMCIRHFYKMLRSGS 183
 QY 399 SKMAARTGVPLASAFPHBYLVSVPLRMFLMAFTGMAAQIPLAFVGRFQNGYGNAAV 457
 DB 184 NKMAARTGVPLASAFPHBYLVSVPLRMFLMAFTGMAAQIPLAFVGRFQNGYGNAAV 242

Search completed: May 5, 2006, 12:33:32
 Job time : 234 secs

RESULT 15
 Q91YB5_RAT PRELIMINARY; PRT; 242 AA.
 ID Q91YB5_RAT PRELIMINARY; PRT; 242 AA.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 5, 2006, 12:27:56 ; Search time 88 Seconds
(without alignments)
2436.555 Million cell updates/sec

Title: US-10-659-800-6
Perfect score: 2594
Sequence: 1 MDRGSSRRRTGRSPSSHG.....VLMYHDDYVLYNPAAPAEA 488

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

. Listing first 45 summaries

Database :

1: A_Geneseq_21:*
2: geneseqp19808:*
3: geneseqp19908:*
4: geneseqp20008:*
5: geneseqp20018:*
6: geneseqp20028:*
7: geneseqp20038:*
8: geneseqp20048:*
9: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2594	100.0	488	3	AA015200 Human ACN
2	2594	100.0	488	8	AD000389 Human dia
3	2594	100.0	488	8	AD084845 Human dia
4	2588	99.8	488	7	ADD45554 Human Pro
5	2588	99.8	488	7	AD059053 Human Pro
6	2588	99.8	488	8	ABW81016 Tumour-as
7	2588	99.8	488	8	AD039678 Human myo
8	2588	99.8	488	8	AD039678 Human myo
9	2299.5	88.6	500	3	AA154139 Acyl-CoA:
10	2299.5	88.6	500	3	AA154139 Acyl-CoA:
11	2292.5	88.4	489	5	AA024973 Bovine DG
12	2286.5	88.1	489	5	AA024973 Bovine di
13	2278.5	87.8	489	6	AD096046 Bovine DG
14	2278.5	87.8	489	6	AD016606 Mouse dig
15	2278.5	87.8	489	8	AD000390 Mouse dia
16	2278.5	87.8	489	8	AD084846 Mouse dia
17	2278.5	87.6	489	8	AA045622 Mouse dia
18	2273.5	87.6	489	6	AD096045 Bovine DG
19	2266.5	87.4	489	7	AD059051 Rat Prote
20	2266.5	87.4	489	7	AD045552 Rat Prote
21	2266.5	87.4	489	8	AD084847 Rat diacy
22	2264	87.3	497	8	AA094523 Bovine dia
23	2192.5	84.5	467	5	AA024974 Bovine di
24	2148	82.8	407	2	AAW43406 Human acy

25	2046	78.9	387	8	AD039677 Human myo
26	2039	78.6	386	3	AA04561 Human dia
27	1681	64.8	421	8	AD035335 ENZM prot
28	1681	64.8	421	8	AD039679 Human myo
29	1297	50.0	236	4	AB010191 Human cdn
30	1297	50.0	236	5	AD066778 Human pol
31	1159	44.7	219	2	AAW43412 Human acy
32	1106	42.6	496	3	AA054140 Acyl-CoA:
33	1106	42.6	496	3	AA019741 Caenorhab
34	1106	42.6	496	8	AD023832 Bacterial
35	1106	42.6	496	8	AD023831 Bacterial
36	834	32.2	538	8	AD080111 Plant ful
37	832.5	32.1	496	8	AD011508 Soybean d
38	819	31.6	507	9	AD016878 Euonymus
39	819	31.6	507	9	AD016893 Euonymus
40	807	31.1	508	3	AA094522 Wheat dia
41	800.5	30.9	504	3	AA094519 Soybean d
42	798.5	30.8	520	3	AA094512 Arabidops
43	797	30.7	532	8	AD081158 Tobacco d
44	797	30.7	532	8	AD081145 Tobacco d
45	791.5	30.5	520	3	AA054143 Acyl-CoA:

ALIGNMENTS

RESULT 1
AA015200 standard, protein, 488 AA.
ID AA015200 standard, protein, 488 AA.
AC AA015200;
XX
XX
DT 14-DEC-2000 (first entry)
XX
DE Human ACAT Related Gene Product 1 ACAT1.
XX
KW Human; ACAT Related Gene Product 1; ACAT1; gene therapy; enzyme;
KW acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1;
KW sterol esterification; lipid homeostasis; diacylglycerol acyltransferase;
KW DGAT; cholesterol; triglyceride biosynthesis; hypertriglyceridaemia;
KW hyperlipidaemia; atherosclerosis; heart disease; obesity.
XX
OS Homo sapiens.
XX
PN US6100077-A.
XX
PD 08-AUG-2000.
XX
PF 01-OCT-1998; 98US-00165042.
XX
PP 01-OCT-1998; 98US-00165042.
XX
PR 01-OCT-1998; 98US-00165042.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Sturley SL, Oelkers P;
XX
XX MPI: 2000-557622/51.
XX N-ESDB; AA076169.
XX
PT New nucleic acid encoding a human diacylglycerol acyltransferase, useful
PT for treating hyperlipidemia, atherosclerosis, heart disease, or other
PT diseases associated with an imbalance of triglyceride levels.
XX
PS Claim 1; Fig 1A; 32bp; English.
XX
XX The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACAT1) mediates
XX sterol esterification, an important component of intracellular lipid
XX homeostasis. The present sequence is human ACAT Related Gene Product 1
XX (ACAT1). This enzyme is a diacylglycerol acyltransferase (DGAT). This
XX enzyme does not esterify cholesterol. It is thought therefore that ACAT1
XX participates in the Coenzyme A-dependent acylation of substrate(s) other
XX than cholesterol e.g. diacylglycerol. Also, ACAT1 has a predicted
XX diacylglycerol binding motif, suggesting that it may perform the last

CC acylation in triglyceride biosynthesis. ACP1 gene and protein are useful
CC for treating a subject who has an imbalance in triglyceride levels due to
CC a defect in esterification of diacylglycerol via gene therapy. Particularly,
CC ACP1 is useful for treating hypertriglyceridaemia, hyperlipidaemia,
CC atherosclerosis, heart disease, obesity or other diseases associated with
CC high or excessive levels of triglyceride

XX Sequence 488 AA:

Query Match 100.0%; Score 2594; DB 3; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.4e-273;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDGSSRRRTGSPSSHGCGGPAABEVDAAAGDPVGAAGAPAPAPAKKODAGVG 60
DB 1 MGDGSSRRRTGSPSSHGCGGPAABEVDAAAGDPVGAAGAPAPAPAKKODAGVG 60
QY 61 SGHWELRCHRLQDSLFSDDSGFSNRYGILNMCVWMLISNARLPLENLIKYGILVDP1QV 120
DB 61 SGHWELRCHRLQDSLFSDDSGFSNRYGILNMCVWMLISNARLPLENLIKYGILVDP1QV 120
QY 121 VSLFKDPSHPAPCLVIAANFAVAARQVEKRLAVGALTBOAGLLHVANLATTLCPPA 180
DB 121 VSLFKDPSHPAPCLVIAANFAVAARQVEKRLAVGALTBOAGLLHVANLATTLCPPA 180
QY 181 AVVLIVESTITPVGSLALMAHTILFLKLFYRDVNSWCRARAKAASAGKASAAAPHT 240
DB 181 AVVLIVESTITPVGSLALMAHTILFLKLFYRDVNSWCRARAKAASAGKASAAAPHT 240
QY 241 VSYPDNLTYRDLYYFLFAPTLCEYNLPPRSRIRKRLRILEMLFTQLOVGILQOMM 300
DB 241 VSYPDNLTYRDLYYFLFAPTLCEYNLPPRSRIRKRLRILEMLFTQLOVGILQOMM 300
QY 301 VPTIIONSKPKPKMDYSRIIERLKLAVPNHILMIFPYWLFHSCINAAVAELMOPGDBEF 360
DB 301 VPTIIONSKPKPKMDYSRIIERLKLAVPNHILMIFPYWLFHSCINAAVAELMOPGDBEF 360
QY 361 YRDWNSSESVTFMQWNMI PVHKCIRHFYKPMRLRGSSKMMARQVFLASAFHEIYVS 420
DB 361 YRDWNSSESVTFMQWNMI PVHKCIRHFYKPMRLRGSSKMMARQVFLASAFHEIYVS 420
QY 421 VPLRMFLMAFTGMAAQIPLAMFVGRFPGNGYNAAVMLSLITGPIAVLAMYVDYYVLN 480
DB 421 VPLRMFLMAFTGMAAQIPLAMFVGRFPGNGYNAAVMLSLITGPIAVLAMYVDYYVLN 480
QY 481 YEAPAAEA 488
DB 481 YEAPAAEA 488

RESULT 2

ADS00389 ID ADS00389 standard; protein; 488 AA.

XX ADS00389;

XX 16-DEC-2004 (first entry)

XX Human diacylglycerol acyltransferase 1.

XX Antifateriosclerotic; Antilipemic; Antidiabetic; Anorectic; Cardiant;
KW diacylglycerol acyltransferase-1; glucose; cholesterol; triglyceride;
KW lipid metabolism; cholesterol metabolism; atherosclerosis;
KW hyperlipidaemia; diabetes; type 2 diabetes; obesity;
KW cardiovascular disease; human; enzyme.

XX Homo sapiens.

XX US2004185559-A1.

XX 23-SEP-2004.

XX

PF 21-MAR-2003; 2003US-00394808.

XX 21-MAR-2003; 2003US-00394808.

PA (ISIS-) ISIS PHARM INC.

PI Monta BP, Graham MJ;

DR MPI: 2004-667979/65.

DR N-PSDB; ADS00240.

PT New antisense oligonucleotides targeted to diacylglycerol acyltransferase
PT 1, useful for treating diacylglycerol acyltransferase 1-associated
PT diseases or conditions, e.g. atherosclerosis, hyperlipidemia, diabetes or
PT obesity.

PS Disclosure; Page 27-29; 55pp; English.

CC The invention relates to a compound targeted to a nucleic acid molecule
CC encoding diacylglycerol acyltransferase 1. The compound is useful for
CC treating a disease or condition associated with diacylglycerol
CC acyltransferase 1; modulating glucose or cholesterol levels, or lowering
CC triglyceride levels in an animal; or for delaying the onset of a disease
CC or condition associated with diacylglycerol acyltransferase 1 in an
CC animal, such as abnormal lipid metabolism, abnormal cholesterol
CC metabolism, atherosclerosis, abnormal metabolic condition,
CC hyperlipidaemia, diabetes, type 2 diabetes, obesity, cardiovascular
CC disease. The present sequence represents the amino acid sequence of human
CC diacylglycerol acyltransferase 1.

SQ Sequence 488 AA:

Query Match 100.0%; Score 2594; DB 8; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.4e-273;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDGSSRRRTGSPSSHGCGGPAABEYRDAAAGDPVGAAGAPAPAPAKKODAGVG 60
DB 1 MGDGSSRRRTGSPSSHGCGGPAABEYRDAAAGDPVGAAGAPAPAPAKKODAGVG 60
QY 61 SGHWELRCHRLQDSLFSDDSGFSNRYGILNMCVWMLISNARLPLENLIKYGILVDP1QV 120
DB 61 SGHWELRCHRLQDSLFSDDSGFSNRYGILNMCVWMLISNARLPLENLIKYGILVDP1QV 120
QY 121 VSLFKDPSHPAPCLVIAANFAVAARQVEKRLAVGALTBOAGLLHVANLATTLCPPA 180
DB 121 VSLFKDPSHPAPCLVIAANFAVAARQVEKRLAVGALTBOAGLLHVANLATTLCPPA 180
QY 181 AVVLIVESTITPVGSLALMAHTILFLKLFYRDVNSWCRARAKAASAGKASAAAPHT 240
DB 181 AVVLIVESTITPVGSLALMAHTILFLKLFYRDVNSWCRARAKAASAGKASAAAPHT 240
QY 241 VSYPDNLTYRDLYYFLFAPTLCEYNLPPRSRIRKRLRILEMLFTQLOVGILQOMM 300
DB 241 VSYPDNLTYRDLYYFLFAPTLCEYNLPPRSRIRKRLRILEMLFTQLOVGILQOMM 300
QY 301 VPTIIONSKPKPKMDYSRIIERLKLAVPNHILMIFPYWLFHSCINAAVAELMOPGDBEF 360
DB 301 VPTIIONSKPKPKMDYSRIIERLKLAVPNHILMIFPYWLFHSCINAAVAELMOPGDBEF 360
QY 361 YRDWNSSESVTFMQWNMI PVHKCIRHFYKPMRLRGSSKMMARQVFLASAFHEIYVS 420
DB 361 YRDWNSSESVTFMQWNMI PVHKCIRHFYKPMRLRGSSKMMARQVFLASAFHEIYVS 420
QY 421 VPLRMFLMAFTGMAAQIPLAMFVGRFPGNGYNAAVMLSLITGPIAVLAMYVDYYVLN 480
DB 421 VPLRMFLMAFTGMAAQIPLAMFVGRFPGNGYNAAVMLSLITGPIAVLAMYVDYYVLN 480
QY 481 YEAPAAEA 488
DB 481 YEAPAAEA 488

RESULT 3
 ADS84845
 ID ADS84845 standard; protein; 488 AA.
 XX
 AC ADS84845;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Human diacylglycerol acyltransferase 1 (DGAT1).
 XX
 KM antihypertensive; antiarteriosclerotic; antidiabetic; anorectic;
 KM cardiovascular; gene therapy; DGAT-Modulator-1; DGAT-Inhibitor-1;
 KM diacylglycerol acyltransferase 1; DGAT1; gene expression;
 KM DGAT1 modulator; cholesterol; glucose level; insulin level;
 KM glucose tolerance; insulin tolerance; lipid metabolism;
 KM cholesterol; metabolism; atherosclerosis; abnormal metabolic condition;
 KM hyperlipidaemia; diabetes; Type 2 diabetes; obesity;
 KM cardiovascular disease; human.
 XX
 OS Homo sapiens.
 XX
 PN US2004209838-A1.
 XX
 PD 21-OCT-2004.
 XX
 PF 18-MAR-2004; 2004US-00803482.
 XX
 PR 21-MAR-2003; 2003US-00394808.
 XX
 PA (MONI/) MONIA B P.
 PA (GRAH/) GRAHAM M J.
 XX
 PI Monica BP, Graham MJ;
 XX
 DR WPI: 2004-747287/73.
 DR N-PsDB; ADS84617.
 XX
 PT New compound 8-80 nucleobases in length targeted to a nucleic acid
 PT molecule encoding diacylglycerol acyltransferase 1 (DGAT1), useful for
 PT treating an animal having e.g., atherosclerosis, hyperlipidaemia,
 PT diabetes, or obesity.
 PT
 PS Disclosure; Page 34-36; 77pp; English.
 XX
 CC The invention describes a compound 8 to 80 nucleobases in length targeted
 CC to a nucleic acid molecule encoding diacylglycerol acyltransferase 1
 CC (DGAT1), where the compound specifically hybridises with the nucleic acid
 CC molecule encoding DGAT1 comprising a sequence comprising 1976 bp (SEQ ID
 CC NO: 4) fully defined in the specification, and inhibits the expression of
 CC DGAT1. Also described are: inhibiting the expression of DGAT1 in cells or
 CC tissues; screening for a modulator of DGAT1; a diagnostic method for
 CC identifying a disease state; a kit or assay device comprising the
 CC compound above; modulating glucose levels in an animal; preventing or
 CC delaying the onset of a disease or condition associated with DGAT1 in an
 CC animal; modulating cholesterol levels in an animal; reducing serum
 CC glucose levels; DGAT1 levels in the liver; circulating insulin levels;
 CC decreasing fasted serum insulin levels; improving an animal's performance
 CC on glucose tolerance tests and insulin tolerance tests; reducing
 CC circulating triglycerides, liver triglycerides or free fatty acids in the
 CC liver of an animal; and lowering triglyceride levels in an animal. The
 CC compound is useful in a method for treating an animal having a disease or
 CC condition associated with DGAT1, i.e., abnormal lipid metabolism,
 CC abnormal cholesterol metabolism, atherosclerosis, abnormal metabolic
 CC condition (i.e., hyperlipidaemia), diabetes (i.e., Type 2 diabetes),
 CC obesity, or cardiovascular disease, so that expression of DGAT1 is
 CC inhibited. This is the amino acid sequence of human diacylglycerol
 CC acyltransferase 1 (DGAT1).
 XX
 SQ Sequence 488 AA;

QY 1 MGDGSSRRRTGSRPSSHGGGPPAAAEVEVDAAAGPDVGAAGAPAPAPKDGDAVG 60
 DB 1 MCDRGSSRRRTGSRPSSHGGGPPAAAEVEVDAAAGPDVGAAGAPAPAPKDGDAVG 60
 QY 61 SGHWEIRCHRLQDSLFSSDSGFSNRYGILMVCVWLISNARLPLENLIKYGIIVDP1QV 120
 DB 61 SGHWEIRCHRLQDSLFSSDSGFSNRYGILMVCVWLISNARLPLENLIKYGIIVDP1QV 120
 QY 121 VSLFLKDPHSWAPCLVIAANFAVAFOVEKRLAVGALTDEAGILLHVAANLATTLCFPA 180
 DB 121 VSLFLKDPHSWAPCLVIAANFAVAFOVEKRLAVGALTDEAGILLHVAANLATTLCFPA 180
 QY 181 AVVLVVESTTPVGSLLAAMAHTILFLKLFPSYRDVSWCRBARAKASAGKASAAAPRT 240
 DB 181 AVVLVVESTTPVGSLLAAMAHTILFLKLFPSYRDVSWCRBARAKASAGKASAAAPRT 240
 QY 241 VSPYDNLTYRDLVYELFAPTLCYELNPPRSPIRIRKFLIRLLEMLFFTQIQVGLIQWM 300
 DB 241 VSPYDNLTYRDLVYELFAPTLCYELNPPRSPIRIRKFLIRLLEMLFFTQIQVGLIQWM 300
 QY 301 VPTIIONSKKPFKMDYSRIIERLLKLAVPNHLIWFYVWLFHSLTANVAELMFGDDEF 360
 DB 301 VPTIIONSKKPFKMDYSRIIERLLKLAVPNHLIWFYVWLFHSLTANVAELMFGDDEF 360
 QY 361 YRDMNNSSVTYFMQNMNIPIVHKICIRPFYKPMLEBRGSSKMMARTGVFLAASFPEYLYS 420
 DB 361 YRDMNNSSVTYFMQNMNIPIVHKICIRPFYKPMLEBRGSSKMMARTGVFLAASFPEYLYS 420
 QY 421 VPLRMFRLMAFTGMAAQIPLAMFYGRFPGVGNNAVWLISLIIGPIAVLWVHDYVYLN 480
 DB 421 VPLRMFRLMAFTGMAAQIPLAMFYGRFPGVGNNAVWLISLIIGPIAVLWVHDYVYLN 480
 QY 481 YEAPPAEA 488
 DB 481 YEAPPAEA 488

RESULT 4
 ADD45554
 ID ADD45554 standard; protein; 488 AA.
 AC ADD45554;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein XP_035370, SEQ ID NO 11218.
 XX
 KM Human; pain; neuronal tissue; gene therapy;
 KM spinal segmental nerve injury; chronic constriction injury; CCI;
 KM spared nerve injury; SNF; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GHEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR WPI: 2003-268312/26.
 DR GENBANK; XP_035370.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page: 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 488 AA;

XX Query Match 99.8%; Score 2588; DB 7; Length 488;

XX Best Local Similarity 99.8%; Pred. No. 1.1e-272;

XX Matches 487; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 1 MGDRSSRRRTGSPSSHGGGPPAAAEVEVDAAAGPVGAAADPAPAPAPKDDAGVG 60
QY 1 SGMWELRCHRLDLSFSSDSGFSNYRGILMVCVWLILSNARLFLENTIKYGIIVDP1QV 120
DB 61 SGMWELRCHRLDLSFSSDSGFSNYRGILMVCVWLILSNARLFLENTIKYGIIVDP1QV 120
QY 121 VSLFLKDHSPAPCLVTAANFANAARQVEKRLAVGALTBEQAGLLHVAANLATTLCPPA 180
DB 121 VSLFLKDEYSWPAFLVIAANFAAARQVEKRLAVGALTBEQAGLLHVAANLATTLCPPA 180
QY 181 AVLLVESITPVGSLALMAHTILFLKFSYRDVNSWCRBARAKASAGKSSAAAPHT 240
DB 181 AVLLVESITPVGSLALMAHTILFLKFSYRDVNSWCRBARAKASAGKSSAAAPHT 240
QY 241 VSYPNLTYYRDLYYFLFAPTLCEYELNFPSPRIRKRLRLILEMLFTQLQVGLIQWM 300
DB 241 VSYPNLTYYRDLYYFLFAPTLCEYELNFPSPRIRKRLRLILEMLFTQLQVGLIQWM 300
QY 301 VPTIIONSKKPPKDMYSRIERLLKLAIVNHLIWLIFFWMLFHSLCLNAVAELMOGDEEF 360
DB 301 VPTIIONSKKPPKDMYSRIERLLKLAIVNHLIWLIFFWMLFHSLCLNAVAELMOGDEEF 360
QY 361 YRDWNSSSVYTFQNMNIPVHKWCI RHPYKPM LRGSSKMAARGVFLASAFPEHYVS 420
DB 361 YRDWNSSSVYTFQNMNIPVHKWCI RHPYKPM LRGSSKMAARGVFLASAFPEHYVS 420
QY 421 VPLRMFLMAFTGMAAQIPLAWFVGRFQNGYNAAWLSLIIIGQPIAVLMTVHDYYVLN 480
DB 421 VPLRMFLMAFTGMAAQIPLAWFVGRFQNGYNAAWLSLIIIGQPIAVLMTVHDYYVLN 480
QY 481 YEAPAAEA 488
DB 481 YEAPAAEA 488

RESUT 5
ADES9053
ID ADES9053 standard; protein; 488 AA.

AC ADES9053;

DT 29-JAN-2004 (first entry)

DE Human Protein XP_035370, SEQ ID NO 4944.

KM Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KX spared nerve injury; SNI; Chung.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

XX MPI; 2003-268312/26.

DR GENBANK; XP_035370.

XX New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

PT Claim 1; Page: 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

XX or human polynucleotides or a polynucleotide which represents a fragment,

XX derivative or allelic variation of the nucleic acid sequence. Also

XX claimed are a vector comprising the novel polynucleotide, a host cell

XX comprising the vector, a method for identifying a nucleotide sequence

XX which is differentially regulated in an animal subjected to pain and a

XX kit to perform the method, an array, a method for identifying an agent

XX that increases or decreases the expression of the polynucleotide sequence

XX that is differentially expressed in neuronal tissue of a first animal

XX subjected to pain, a method for identifying a compound which regulates

XX the expression of a polynucleotide sequence which is differentially

XX expressed in an animal subjected to pain, a method for identifying a

XX compound that regulates the activity of one or more of the

XX polynucleotides, a method for producing a pharmaceutical composition, a

XX method for identifying a compound or small molecule that regulates the

XX activity in an animal of one or more of the polypeptides given in the

XX specification, a method for identifying a compound useful in treating

XX pain and a pharmaceutical composition comprising the one or more

XX polypeptides or their antibodies. The polynucleotide or the compound that

XX modulates its activity is useful for preparing a medicament for treating

XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

XX therapy). The sequence presented is a human protein (shown in Table 2 of

XX the specification) which is differentially expressed during pain. Note:

XX The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic form directly from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 488 AA;

XX Query Match 99.8%; Score 2588; DB 7; Length 488;

XX Best Local Similarity 99.8%; Pred. No. 1.1e-272;

AD039676
ID AD039676 standard; protein; 488 AA.
XX
AC AD039676;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1339.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin J, Iakubova O;
XX
DR WPI; 2004-533949/51.
XX
DR N-PSDB; AD038848.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1339; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acid of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 488 AA;

Query Match 99.8%; Score 2588; DB 8; Length 488;
Best Local Similarity 99.8%; Pred. No. 1.1e-272;
Matches 487; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MGDGSSRRRTGSRPSSHGCGGPAABEEVDAAGDPVGAADPAAPAPNKGDAVG 60

|||||
Db 1 MGDGSSRRRTGSRPSSHGCGGPAABEEVDAAGDPVGAADPAAPAPNKGDAVG 60
QY 61 SGHWEIRCHRIQDSLFSDDSGFSNRYGILNMCVMTLISNARPLENLIKXGIIIVDPYQV 120
Db 61 SGHWEIRCHRIQDSLFSDDSGFSNRYGILNMCVMTLISNARPLENLIKXGIIIVDPYQV 120
QY 121 VSLFLKDPHSWPAPCLVAAAVFAVAAFOVEKRLAVGALTQAGLLHVNIAATILCPFA 180
Db 121 VSLFLKDPHSWPAPCLVAAAVFAVAAFOVEKRLAVGALTQAGLLHVNIAATILCPFA 180
QY 181 AVVLIVESITPVGSLIAIMAHITILFLKFSYRDVNSWCRARARAKAASAGKKAASAAAPHT 240
Db 181 AVVLIVESITPVGSLIAIMAHITILFLKFSYRDVNSWCRARARAKAASAGKKAASAAAPHT 240
QY 241 VSYPDNLTLYRDLYFLFAPILCYELNFPSPRIKRFILRRILMLPFTQLOVGLIOQM 300
Db 241 VSYPDNLTLYRDLYFLFAPILCYELNFPSPRIKRFILRRILMLPFTQLOVGLIOQM 300
QY 301 VPTIIONSMKPKMDYSRIIRLLKLAVPNHLIWLIFPYWLFHSCINAVAEIMQFGDREF 360
Db 301 VPTIIONSMKPKMDYSRIIRLLKLAVPNHLIWLIFPYWLFHSCINAVAEIMQFGDREF 360
QY 361 YRDWNNSESVTYFWQNNNI PVHKWCIRHFYKPLRSGSSKMMARTGVFLASAFHEHYLV 420
Db 361 YRDWNNSESVTYFWQNNNI PVHKWCIRHFYKPLRSGSSKMMARTGVFLASAFHEHYLV 420
QY 421 VPLRMFRLMAFTGMAAOPLAMFVGRFQGYGNAAVLSTIGOPTAVLMVYVDYVYN 480
Db 421 VPLRMFRLMAFTGMAAOPLAMFVGRFQGYGNAAVLSTIGOPTAVLMVYVDYVYN 480
QY 481 YEAPAAEA 488
Db 481 YEAPAAEA 488

RESULT 8
AD039678
ID AD039678 standard; protein; 488 AA.
XX
AC AD039678;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1341.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin J, Iakubova O;
XX
DR WPI; 2004-533949/51.
XX
DR N-PSDB; AD038850.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX

PS Claim 10; SEQ ID NO 1341; 145bp; English.

XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 488 AA;

Query Match 99.8%; Score 2568; DB 8; Length 488;

Best Local Similarity 99.8%; Pred. No. 1.1e-272; Matches 487; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDGSSRRRTGSPSSSHGCGPAAAEERVDAAAGPVGAAGAPAPAPKDGAGVG 60
DB 1 MGDGSSRRRTGSPSSSHGCGPAAAEERVDAAAGPVGAAGAPAPAPKDGAGVG 60
QY 61 SGHWELRCHRLQDSLFFSSDSGFSNYRGILNMCVWMLISNARLPLENLIKYGILVDP1QV 120
DB 61 SGHWELRCHRLQDSLFFSSDSGFSNYRGILNMCVWMLISNARLPLENLIKYGILVDP1QV 120
QY 121 VSLFKDHSWAPCLVTAANFAVAARQVEKRLAVGALTTEQAGLLHVAANTATLCPFA 180
DB 121 VSLFKDHSWAPCLVTAANFAVAARQVEKRLAVGALTTEQAGLLHVAANTATLCPFA 180
QY 181 AVVLVESITPVGSLAAMAHTILFLKLFYRDVNSWCRBARAKASAGKASAAAPT 240
DB 181 AVVLVESITPVGSLAAMAHTILFLKLFYRDVNSWCRBARAKASAGKASAAAPT 240
QY 241 VSYDNLTYRDLTYFLFAFTLCYELNPPRSPRIKRRFLRLILEMLFTQLQVGIQOMW 300
DB 241 VSYDNLTYRDLTYFLFAFTLCYELNPPRSPRIKRRFLRLILEMLFTQLQVGIQOMW 300
QY 241 VSYDNLTYRDLTYFLFAFTLCYELNPPRSPRIKRRFLRLILEMLFTQLQVGIQOMW 300
DB 241 VSYDNLTYRDLTYFLFAFTLCYELNPPRSPRIKRRFLRLILEMLFTQLQVGIQOMW 300
QY 301 VPTIÖNSMKPFPKDMYSRILIERLLKLAVPNHLIMLIFPWLPHSCLNAAELMOGDRBF 360
DB 301 VPTIÖNSMKPFPKDMYSRILIERLLKLAVPNHLIMLIFPWLPHSCLNAAELMOGDRBF 360
QY 361 YRDWNSSESVTYFMQNMNIPVHKWCIRHFPYKPMLERRGSSKMAARTGVFLASAPFEYLV 420
DB 361 YRDWNSSESVTYFMQNMNIPVHKWCIRHFPYKPMLERRGSSKMAARTGVFLASAPFEYLV 420
QY 421 VPLERFLMAFTGMAAQIPLAWFVRFPQNGYGNAAWMLSLITIGPIAVLMTVHDYYVLN 480
DB 421 VPLERFLMAFTGMAAQIPLAWFVRFPQNGYGNAAWMLSLITIGPIAVLMTVHDYYVLN 480
QY 481 YEAPAAEA 488
DB 481 YEAPAAEA 488

RESULT 9
AA54139
ID AA54139 strand; protein; 500 AA.

XX AC AA54139;

XX 27-MAR-2000 (first entry)

XX Acyl-CoA:cholesterol acyltransferase (ACAT)-like protein.

XX Acyl-CoA:cholesterol acyltransferase; ACAT; ACAT-like protein; sterol;
XX ester; triacylglycerol; fatty acyl-CoA; lipid composition; plant cell;
XX diacylglycerol acyltransferase; DAGAT; triglyceride; cancer; diabetes;
XX cardiopulmonary disease; heart failure; atherosclerosis; adipocytosis;
XX leukaemia; skin carcinoma; fibroblastoma; metabolic disorder; obesity;
XX abnormal lipid metabolism; abnormal fat absorption;
XX lipoprotein secretion; adipogenesis.

XX Rattus sp.

XX MO9963096-A2.

XX 09-DEC-1999.

XX 04-JUN-1999; 99WO-US012541.

XX 05-JUN-1998; 98US-0088143P.

XX 12-NOV-1998; 98US-0108389P.

XX (CALJ) CALGENE LLC.

XX Lasener MW, Ruzinskiy DM;

XX WPI, 2000-105701/09.

XX N-PSDB; AA245385.

XX Novel polynucleotides used for modifying plant oil composition and for
XX developing products for treating e.g. cancer, diabetes, cardiopulmonary
XX disease or metabolic disorders.

XX Example 2; Fig 11; 89pp; English.

XX The present sequence represents an acyl-CoA:cholesterol acyltransferase
XX (ACAT) related protein. The ACAT-like protein is active in the formation
XX of a sterol, ester and/or triacylglycerol from a fatty acyl-CoA and
XX sterol and/or diacylglycerol substrate. The DNA can be used for modifying
XX the lipid composition of plant cells. The ACAT-like protein has
XX diacylglycerol acyltransferase (DAGAT) activity, and so the synthesis of
XX triglycerides can be suppressed or increased using the DNA. The protein
XX can be used to produce plant oils with a modified triglyceride content.
XX The products can also be used to identify antagonists and agonists of
XX DAGAT activity. Such agonists and antagonists are particularly useful in
XX treating or ameliorating diseases associated with DAGAT activity.
XX CC including diseases associated with altered cellular diacylglycerol
XX concentration or PKC activity, including cancer, diabetes,
XX cardiopulmonary diseases e.g. heart failure, atherosclerosis,
XX adipocytosis, leukaemia, skin carcinoma, fibroblastoma, metabolic
XX disorders, obesity, diseases associated with abnormal lipid metabolism,
XX CC and diseases associated with abnormal fat absorption, lipoprotein
XX secretion and adipogenesis

XX Sequence 500 AA;

Query Match 88.6%; Score 2299.5; DB 3; Length 500;

Best Local Similarity 85.9%; Pred. No. 3.4e-241; Matches 427; Conservative 26; Mismatches 31; Indels 13; Gaps 3;

QY 1 MGDGSSRRRTGSPSSSHGCGPAAAEERVDAAAGPVGAAGAPAPAPKDGAGVG 51
DB 1 MGDGSSRRRTGSPSSSHGCGPAAAEERVDAAAGPVGAAGAPAPAPKDGAGVG 60
QY 52 --NKDGDAGVSGHWELRCHRLQDSLFFSSDSGFSNYRGILNMCVWMLISNARLPLENLIK 109
DB 52 --NKDGDAGVSGHWELRCHRLQDSLFFSSDSGFSNYRGILNMCVWMLISNARLPLENLIK 109

Db TRDKDQRTSVGDGHWEELRCHRLQDSLFSDDSGFSNVRGILMNCVMTLISNARLFLENLI 120
Qy 110 KYGILVDPPIQVVSLEFLKDPHSPAPCLVIAANVFAVAFOVEKRLAVGALTEOAGLLHV 169
Db 121 KYGILVDPPIQVVSLEFLKDPHSPAPCLVIAANVFAVAFOVEKRLAVGALTEOAGLLHV 180
Qy 170 ANLATILCFPAVAVLVESITPVGSLALMAHTILFLKLSYRDVNSWC--RRARAKAS 227
Db 181 VNLATILCFPAVAVLVESITPVGSLFALASYSITFLKLSYRDVNLWCROQRVAKAVS 240
Qy 228 AGKASSAAAPHTVSYPNLTYYRDLVYFLFAPTLCEYELNFRSPRIKRRFLRLLEMLF 287
Db 241 AGKAVSGAAQNTVSYPNLTYYRDLVYFLFAPTLCEYELNFRSPRIKRRFLRLLEMLF 300
Qy 288 FTQLOVGLIQOMVPTIONSMPKPFDMYSRILIELRLKLAVPNHLIWLIFPYWLFHSCIN 347
Db 301 FTQLOVGLIQOMVPTIONSMPKPFDMYSRILIELRLKLAVPNHLIWLIFPYWLFHSCIN 360
Qy 348 AVAELMOFGDREFFYRDWNNSESVTYFWQNNMIPVHKWCIRHFYKPMRLRGSSKMMARTGV 407
Db 361 AVAELMOFGDREFFYRDWNNSESVTYFWQNNMIPVHKWCIRHFYKPMRLRGSSKMMARTGV 420
Qy 408 FLASAFHEHYLVSPILRMFRMAFTGMAQIPLAMFVGRFPOGNYGNAAVVLTLLIGQPI 467
Db 421 FLASAFHEHYLVSPILRMFRMAFTGMAQIPLAMFVGRFPOGNYGNAAVVLTLLIGQPI 480
Qy 468 AVLMTVHDYVYLVANVEAP 484
Db 481 AVLMTVHDYVYLVANVEAP 497

RESULT 10

AAB19742 standard; protein; 500 AA.

AA19742;

19-FEB-2001 (first entry)

Rat acyl CoA:cholesterol acyltransferase.

Acyl CoA:cholesterol acyltransferase; ACAT; transgenic plant; sterol;
tocopherol; phytosterol; phytoestanol; anticholesterolemic; hypolipemic;
rat.

Rattus sp.

MO200061771-A2.

19-OCT-2000.

12-APR-2000; 2000MO-US009696.

12-APR-1999; 99US-0128995P.

(MONS) MONSANTO CO.

Venkatesh M, Corbin DR, Bhat GB, Boddupalli SS, Grebenok RJ,
Kishore GM, Lardizabal KD, Lasser MW, Rangwala SH, Karunananda B,
WPI; 2000-665136/64.
DR N-PSDB; AAA88846.

Genetically engineering the biosynthetic pathways in plants involved in
the accumulation of sterol compounds and tocopherol to produce compounds
for lowering the level of low density lipoprotein cholesterol in blood
serum.

Disclosure; Page 64; 166pp; English.

The present sequence is that of rat acyl CoA:cholesterol acyltransferase
(ACAT), as deduced from ACAT DNA (see AAA88846). Sterol O-
acyltransferases such as ACAT catalyse the formation of cholesterol

esters from cholesterol and long chain fatty acids. Recombinant
constructs of the invention are used to alter the biosynthesis and
accumulation of sterols and tocopherols in transgenic plants. Seeds of
such plants may contain elevated levels of sitosterol and/or its esters,
and alpha-tocopherol, and reduced levels of campesterol and campestanol
CC and their esters. The seeds may also contain the novel sterol
CC brassicasteranol. Oil obtained from the seeds can be used in food and
pharmaceutical compositions to lower levels of low density lipoprotein
cholesterol in blood serum. ACAT enzymes can be used in the present
invention to produce elevated levels of phytosterol and/or phytosteranol
esters

Sequence 500 AA;

Query Match 88.6%; Score 2299.5; DB 3; Length 500;
Best Local Similarity 85.9%; Pred. No. 3.4e-241;
Matches 427; Conservative 26; Mismatches 31; Indels 13; Gaps 3;

Qy 1 MGDR---GSSRRRTGSRPSHGGGPPAAEEVRAAAGDVGAGAPAPAPAPAPAPAPAPAPAP 51
Db 1 MGDRGAGASSRRRTGSRVSIQGGSGPWVDEEVRDAVGPDLGAGDAPAPAPAPAPAPAPAP 60
Qy 52 --NKDGAAGVSGHWEELRCHRLQDSLFSDDSGFSNVRGILMNCVMTLISNARLFLENLI 109
Db 61 TRDKDQRTSVGDGHWEELRCHRLQDSLFSDDSGFSNVRGILMNCVMTLISNARLFLENLI 120
Qy 110 KYGILVDPPIQVVSLEFLKDPHSPAPCLVIAANVFAVAFOVEKRLAVGALTEOAGLLHV 169
Db 121 KYGILVDPPIQVVSLEFLKDPHSPAPCLVIAANVFAVAFOVEKRLAVGALTEOAGLLHV 180
Qy 170 ANLATILCFPAVAVLVESITPVGSLALMAHTILFLKLSYRDVNSWC--RRARAKAS 227
Db 181 VNLATILCFPAVAVLVESITPVGSLFALASYSITFLKLSYRDVNLWCROQRVAKAVS 240
Qy 228 AGKASSAAAPHTVSYPNLTYYRDLVYFLFAPTLCEYELNFRSPRIKRRFLRLLEMLF 287
Db 241 AGKAVSGAAQNTVSYPNLTYYRDLVYFLFAPTLCEYELNFRSPRIKRRFLRLLEMLF 300
Qy 288 FTQLOVGLIQOMVPTIONSMPKPFDMYSRILIELRLKLAVPNHLIWLIFPYWLFHSCIN 347
Db 301 FTQLOVGLIQOMVPTIONSMPKPFDMYSRILIELRLKLAVPNHLIWLIFPYWLFHSCIN 360
Qy 348 AVAELMOFGDREFFYRDWNNSESVTYFWQNNMIPVHKWCIRHFYKPMRLRGSSKMMARTGV 407
Db 361 AVAELMOFGDREFFYRDWNNSESVTYFWQNNMIPVHKWCIRHFYKPMRLRGSSKMMARTGV 420
Qy 408 FLASAFHEHYLVSPILRMFRMAFTGMAQIPLAMFVGRFPOGNYGNAAVVLTLLIGQPI 467
Db 421 FLASAFHEHYLVSPILRMFRMAFTGMAQIPLAMFVGRFPOGNYGNAAVVLTLLIGQPI 480
Qy 468 AVLMTVHDYVYLVANVEAP 484
Db 481 AVLMTVHDYVYLVANVEAP 497

RESULT 11

AAB24973 standard; protein; 489 AA.

AAE24973;

22-OCT-2002 (first entry)

Bovine DGAT1 protein.

Bovine; diacylglycerol acyltransferase; genotyping; milk production;
DGAT1; polymorphism; farming industry; transgenic; chromosome 14; enzyme.

Bos taurus.

MO200236824-A1.

10-MAY-2002.

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XX 31-OCT-2001; 2001WO-NZ000245.
PF
XX
XX 31-OCT-2000; 2000NZ-00507888.
PR
XX 06-DEC-2000; 2000NZ-00508662.
PR
XX
XX (GEOR/) GEORGES M A J.
PA (COPP/) COPPIETERS W H R.
PA (GRIS/) GRISART B M J.
PA (SNEI/) SNEEL R G.
PA (REID/) REID S J.
PA (FORD/) FORD C A.
PA (SPEL/) SPELMAN R J.
XX
PI Georges MJ, Coppieters WHR, Grisart BMJ, Snell RG, Reid SJ;
PI Ford CA, Spelman RJ;
XX
XX WPI; 2002-500128/53.
DR N-PSDB; AAD40350.
XX
XX
XX Determining genetic merit of a bovine with respect to milk composition
PT and volume for improved milk production, comprises determining the
PT diacylglycerol acyltransferase gene genotypic state of the bovine.
XX
XX
XX Claim 36; Page 68-69; 128pp; English.
PS
XX
XX The invention relates to a method of genotyping bovine for improved milk
CC production traits which comprises determining the diacylglycerol
CC acyltransferase (DGAT1) genotypic state of the bovine, wherein the DGAT1
CC gene and polymorphisms have been found to be associated with such
CC improved milk production traits. The method is useful for selecting a
CC bovine having a desired DGAT1 genotypic state. It is also useful for the
CC identification and selection of a bovine having one of the polymorphisms
CC in its DGAT1 gene. Milk produced from selected bovine which is useful for
CC making a dairy product provides a beneficial health effect. An antibody
CC to the protein having DGAT1 activity is useful for inhibiting the
CC activity of bovine DGAT1 in a lactating bovine so as to modulate milk
CC production and/or milk solids content. DGAT1 nucleic acid and its
CC fragments are useful in the farming industry. They are also useful to
CC generate transgenic animals which are useful to investigate the molecular
CC basis of DGAT1 action and to test a substance for the ability to prevent,
CC slow or enhance DGAT1 activity. The present sequence is bovine DGAT1
CC protein. DGAT1 gene is located on chromosome 14
XX
XX
XX Sequence 489 AA;
SQ
Query Match 88.4%; Score 2292.5; DB 5; Length 489;
Best Local Similarity 88.0%; Pred. No. 1.9e-240;
Matches 434; Conservative 15; Mismatches 31; Indels 13; Gaps 3;
QY 1 MGDR---GSSRRRRRGRSSSHGGGPPAAAEVVDAAAGPVGAAGAPAPAPKDDA 57
DB 1 MGDRCGAGGSSRRRRGRSSPSIQGGSGPPAAAEV-----DVGAGGAPVARDTKDDV 54
QY 58 GVSGGHWELRGRLQDLSFFSSDSGFSNRYGILNMCVWMLISNARLFLENLIKYGILVDP 117
DB 55 DVGSGHWLRCRLQDLSFFSSDSGFSNRYGILNMCVWMLISNARLFLENLIKYGILVDP 114
QY 118 IQVSLFLKDPHSPAPCLVIAANVFAVAFAQVEKRLAAGALTEQAGILLHVAIATLTC 177
DB 115 IQVSLFLKDPHSPAPCLVIAANVFAVAFAQVEKRLAAGALTEQAGILLHVAIATLTC 174
QY 178 PPAAVVLVESITTPVGSILAAHATILFLKFSYVDNUSWCR-----RAVAASGKAS 233
DB 175 PPAAVVLVESITTPVGSILAAHATILFLKFSYVDNUSWCR-----RAVAASGKAS 234
QY 234 SAAPHYTSYDNLTYRDLTYFLFAPTLCEYELNFRSRIRKRFILRLILEMLFTQLOV 293
DB 235 GGAHQRTSYDNLTYRDLTYFLFAPTLCEYELNFRSRIRKRFILRLILEMLFTQLOV 294
QY 294 GLIQGMVPTIQNSMKPFKMDYSRIIRLLKLAVPNHLIWLIFPYWLPHSCLNAVAELM 353
DB 295 GLIQGMVPTIQNSMKPFKMDYSRIIRLLKLAVPNHLIWLIFPYWLPHSCLNAVAELM 354

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QY 354 QGDREFFRDWNNSESVTYFMQNNWNI PVHKNCIRHFYKPMILRGSSKMMARTGTVELASAF 413
DB 355 QGDREFFRDWNNSSITTYFMQNNWNI PVHKNCIRHFYKPMILRGSSKMMARTGTVELASAF 414
QY 414 FHEYLVSVPLEMFRLMAFTGMAQIPLAMFVGRFFQSYGNAVAWMLSLIQGPVILMYV 473
DB 415 FHEYLVSIPLEMFRLMAFTGMAQIPLAMVIGRFRGNYGNAVAWMLSLIQGPVILMYV 474
QY 474 HDYVLANTAEAPPA 486
DB 475 HDYVLNREAPPA 487
RESULT 12
AAE24979
ID AAE24979 standard; protein; 489 AA.
XX
XX AAE24979;
AC
XX
XX 22-OCT-2002 (first entry)
DT
XX
XX Bovine diacylglycerol acyltransferase (DGAT1) mutant, K232A.
DE
XX
XX Bovine; diacylglycerol acyltransferase; genotyping; milk production;
KW DGAT1; polymorphism; farming industry; transgenic; enzyme; mutant;
KW mutain.
XX
XX Bos taurus.
OS
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 232 /note= "Wild-type Lys substituted with Ala"
FT
XX
XX WO200236824-A1.
XX
XX 10-MAY-2002.
XX
XX 31-OCT-2001; 2001WO-NZ000245.
XX
XX 31-OCT-2000; 2000NZ-00507888.
PR 06-DEC-2000; 2000NZ-00508662.
XX
XX (GEOR/) GEORGES M A J.
PA (COPP/) COPPIETERS W H R.
PA (GRIS/) GRISART B M J.
PA (SNEI/) SNEEL R G.
PA (REID/) REID S J.
PA (FORD/) FORD C A.
PA (SPEL/) SPELMAN R J.
XX
PI Georges MJ, Coppieters WHR, Grisart BMJ, Snell RG, Reid SJ;
PI Ford CA, Spelman RJ;
XX
XX WPI; 2002-500128/53.
XX
XX
XX Determining genetic merit of a bovine with respect to milk composition
PT and volume for improved milk production, comprises determining the
PT diacylglycerol acyltransferase gene genotypic state of the bovine.
XX
XX
XX Disclosure; Page; 128pp; English.
PS
XX
XX The invention relates to a method of genotyping bovine for improved milk
CC production traits which comprises determining the diacylglycerol
CC acyltransferase (DGAT1) genotypic state of the bovine, wherein the DGAT1
CC gene and polymorphisms have been found to be associated with such
CC improved milk production traits. The method is useful for selecting a
CC bovine having a desired DGAT1 genotypic state. It is also useful for the
CC identification and selection of a bovine having one of the polymorphisms
CC in its DGAT1 gene. Milk produced from selected bovine which is useful for
CC making a dairy product provides a beneficial health effect. An antibody
CC to the protein having DGAT1 activity is useful for inhibiting the

```

CC activity of bovine DGAT1 in a lactating bovine so as to modulate milk
 CC production and/or milk solids content. DGAT1 nucleic acid and its
 CC fragments are useful in the farming industry. They are also useful to
 CC generate transgenic animals which are useful to investigate the molecular
 CC basis of DGAT1 action and to test a substance for the ability to prevent,
 CC slow or enhance DGAT1 activity. The present sequence is bovine DGAT1
 CC protein mutant used to illustrate the method of the invention. Note: This
 CC sequence is not shown in the specification, however it is constructed
 CC based on the sequence SEQ.ID.NO:2 shown in the sequence listing
 CC (AAE24973)

XX Sequence 489 AA;

Query Match 88.1%; Score 2286.5; DB 5; Length 489;
 Best Local Similarity 87.8%; Pred. No. 8.6e-240;
 Matches 433; Conservative 15; Mismatches 32; Indels 13; Gaps 3;

QY 1 MGDR---GSSRRRTGSRPSSHGSGGPPAAABEEVRDAAAGPDVGAAGAPAPAPNKDGA 57
 DB 1 MGDRGAGGSRRRRTGSRPSSHGSGGPPAAABEEVR-----DVAGAGDAPVADTDKGDV 54
 QY 58 GVGSGHMLRCHRLDLSFSSDSGFSNYRGILNMCVWMLLSNARLFLLENLKYGLVDP 117
 DB 55 DVGSGHMLRCHRLDLSFSSDSGFSNYRGILNMCVWMLLSNARLFLLENLKYGLVDP 114
 QY 118 IQVSLFLKDPHSPAPCLIVANVFAVAAFQVEKRLAVGALTQAGLLHVALNATILC 177
 DB 115 IQVSLFLKDPHSPAPCLIVANVFAVAAFQVEKRLAVGALTQAGLLHVALNATILC 174
 QY 178 FPAAVVLVESITPVGSLIAMAHTILFLKLFSDYDVSNCRR---ARAKASAGKAS 233
 DB 175 FPAAVFLLESITPVGSLIAMAHTILFLKLFSDYDVSNCRRERRRAGAKAKALAGKAN 234
 QY 234 SAAAPHVSYPDNLTLYRDLYFLFAPTLCYELNPPSRIRKRLRLLEMLFTQLOV 293
 DB 235 GGAAGRTVSYPDNLTLYRDLYFLFAPTLCYELNPPSRIRKRLRLLEMLFTQLOV 294
 QY 294 GLIOGMVPTIÖNSMKPKMDYSRIIRLKLAVPNHLIWLFFYWLPHSCLNAVAELM 353
 DB 295 GLIOGMVPTIÖNSMKPKMDYSRIIRLKLAVPNHLIWLFFYWLPHSCLNAVAELM 354
 QY 354 QFGDREPRDWNSSSVTFWQNNANI PVHKWCIRHFYKPMRLRGSSKMMARTGVLASAF 413
 DB 355 QFGDREPRDWNSSSVTFWQNNANI PVHKWCIRHFYKPMRLRGSSKMMARTGVLASAF 414
 QY 414 FHBVIVSVPLMRFLMAFTGMAAOIPLAMFVGRFQGVNNAVWLSLIGPILVLMYV 473
 DB 415 FHBVIVSVPLMRFLMAFTGMAAOIPLAMFVGRFQGVNNAVWLSLIGPILVLMYV 474
 QY 474 HDYVLANEAPPA 486
 DB 475 HDYVLANEAPPA 487

RESULT 13
 ABP96046
 ID ABP96046 standard; protein; 489 AA.
 AC ABP96046;
 DT 07-MAY-2003 (first entry)
 DE Bovine DGAT protein SEQ ID NO:4.
 XX
 XX ACyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14; bovine;
 KM milk; meat marbling; low fat; polymorphic; SNP;
 KM single nucleotide polymorphism.
 OS Bos taurus.
 XX
 XX MO2003004630-A2.
 PD 16-JAN-2003.

XX
 PF 05-JUL-2002; 2002MO-EP007520.
 XX
 PR 06-JUL-2001; 2001EP-00116412.
 PR 13-MAY-2002; 2002US-0379412P.
 XX
 PA (ABBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.
 XX
 PI Fries H, Winter A;
 XX
 DR WPI; 2003-239205/23.
 XX
 DR N-PSDB; AB277045.
 PT
 PT New nucleic acid molecule comprising a sequence of an allele of a
 PT polymorphic bovine acyl CoA:diacylglycerol transferase gene useful for
 PT testing a mammal for its predisposition for fat content of milk and for
 PT meat marbling.

Claim 13; Page 90-91; 91pp; English.

The present invention describes a nucleic acid molecule (NA) (i) encoding
 a bovine acyl CoA:diacylglycerol transferase (DGAT) contributing to or
 indicative for low fat content of milk and to low meat marbling
 (intramuscular fat content). Human DGAT is located to chromosome 8, and
 bovine DGAT is located to chromosome 14. (i) is useful for testing a
 mammal for its predisposition for fat content of milk and/or its
 predisposition for meat marbling. The method comprises analysing the gene
 encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide
 polymorphisms (SNPs)) which are connected with the predisposition. The
 nucleotide polymorphisms are located in the coding region of the DGAT
 gene and result in substitution, deletion and/or addition of an amino
 acid sequence of the polypeptide which is encoded by the gene. The
 nucleic acid molecule has at the position 10433 and 10434 of the DGAT
 gene a guanine and a cytosine residue, at position 3343 a cytosine or
 guanine, 11030 a guanine, 11048 a cytosine or thymine and 11093 a
 thymine, which correlate with a predisposition for low fat content of
 milk and low meat marbling. The nucleic acid molecule has at the position
 CC corresponding to position 10433 and 10434 of the DGAT gene two adenine
 CC residues which correlate with a predisposition for high content of milk
 CC and high meat marbling. The nucleotide polymorphisms are located in a
 CC region which is responsible for the regulation of the expression of the
 CC product of the gene encoding DGAT. AB276924 to AB277045 and ABP96035 to
 CC ABP96046 represent sequences used in the exemplification of the present
 CC invention

XX Sequence 489 AA;

Query Match 87.8%; Score 2278.5; DB 6; Length 489;
 Best Local Similarity 87.8%; Pred. No. 6.4e-239;
 Matches 433; Conservative 14; Mismatches 33; Indels 13; Gaps 3;

QY 1 MGDR---GSSRRRTGSRPSSHGSGGPPAAABEEVRDAAAGPDVGAAGAPAPAPNKDGA 57
 DB 1 MGDRGAGGSRRRRTGSRPSSHGSGGPPAAABEEVR-----DVAGAGDAPVADTDKGDV 54
 QY 58 GVGSGHMLRCHRLDLSFSSDSGFSNYRGILNMCVWMLLSNARLFLLENLKYGLVDP 117
 DB 55 DVGSGHMLRCHRLDLSFSSDSGFSNYRGILNMCVWMLLSNARLFLLENLKYGLVDP 114
 QY 118 IQVSLFLKDPHSPAPCLIVANVFAVAAFQVEKRLAVGALTQAGLLHVALNATILC 177
 DB 115 IQVSLFLKDPHSPAPCLIVANVFAVAAFQVEKRLAVGALTQAGLLHVALNATILC 174
 QY 178 FPAAVVLVESITPVGSLIAMAHTILFLKLFSDYDVSNCRR---ARAKASAGKAS 233
 DB 175 FPAAVFLLESITPVGSLIAMAHTILFLKLFSDYDVSNCRRERRRAGAKAKALAGKAN 234
 QY 234 SAAAPHVSYPDNLTLYRDLYFLFAPTLCYELNPPSRIRKRLRLLEMLFTQLOV 293
 DB 235 GGAAGRTVSYPDNLTLYRDLYFLFAPTLCYELNPPSRIRKRLRLLEMLFTQLOV 294
 QY 294 GLIOGMVPTIÖNSMKPKMDYSRIIRLKLAVPNHLIWLFFYWLPHSCLNAVAELM 353

Db 295 GLLIQMVPALIONSMKPKMDYSRIVERLKLAVPNHLIWLIFYYWLFHSCINAAVEIM 354
 QY QGDEPEFRDMNSRVTYFMQNNMI PVHKICIRHFKYKMLRRGSSKMAARTGVLASAF 413
 Db 354 QGDEPEFRDMNSRVTYFMQNNMI PVHKICIRHFKYKMLRRGSSKMAARTGVLASAF 414
 QY 414 FHEVLVSPLMFRMLAFTGMAAQIPLAMFVGRFQGNVGNAAVWLSLIGQPIAVLMVY 473
 Db 415 FHEVLVSPLMFRMLAFTGMAAQIPLAMVIGRFRGNYGNAAVWLSLIGQPIAVLMVY 474
 QY 474 HDYVLTANTAPAA 486
 Db 475 HDYVLTANTAPAA 487
 RESULT 14
 ADCl6606
 ID ADCl6606 standard; protein; 498 AA.
 XX ADCl6606;
 AC
 XX 18-DEC-2003 (first entry)
 DT
 XX Mouse diglyceride acyltransferase (DGAT) protein sequence.
 DE
 XX diacylglycerol O-acyltransferase; diglyceride acyltransferase; DGAT;
 KM triacylglycerol synthesis; intestinal fat absorption;
 KM lipoprotein assembly; fat storage in adipocytes; milk production;
 KM egg production; sperm maturation; hyperlipidaemia;
 KM cardiovascular disease; obesity; diabetes; cancer; neurological disorder;
 KM immunological disorder; sperm count; transgenic plant;
 KM industrial feedstock; transgenic animal; anti-obesity; cardiant;
 KM cyrostatic; antilipemic compound; mouse; murine; enzyme; EC 2.3.1.20.
 KM
 OS Mus musculus.
 XX
 PN MO967268-A1.
 XX
 PD 29-DEC-1999.
 XX
 XX 23-JUN-1999; 99MO-US014245.
 PF
 XX 24-JUN-1998; 98US-00103754.
 PR 09-NOV-1998; 98US-0107771P.
 XX
 PA (RBC) UNITV CALIFORNIA.
 XX
 PI Farese RV, Cases S, Smith S, Erickson SK, Sande E;
 XX
 DR WPI: 2000-147196/13.
 DR N-PSDB; ADCl6605.
 XX
 PT Novel diacylglycerol O-acyltransferase polynucleotides and polypeptides
 used in treatment therapies and production of triacylglycerols.
 XX
 PS Example 1. SEQ ID NO 5; 63pp; English.
 XX
 CC This invention relates to novel diacylglycerol O-acyltransferase
 CC (diglyceride acyltransferase; DGAT; EC 2.3.1.20) nucleotide and protein
 CC sequences. The DGAT enzyme is involved in triacylglycerol synthesis, and
 CC is important in higher eukaryotes for intestinal fat absorption,
 CC lipoprotein assembly, fat storage in adipocytes, milk production, and
 CC possibly egg production and sperm maturation. The DGAT nucleotide
 CC sequences may be useful for identifying DGAT homologues, as a source of
 CC probes and primers, for the identification of expression patterns in
 CC biological specimens, for the preparation of cell or animal models of
 CC DGAT function, and for the preparation of in vitro models of DGAT
 CC function. The invention may also be used for diagnostic screening, for
 CC the treatment of pathological conditions, and for treatment of conditions
 CC related to DGAT expression or activity. Diseases diagnosed and/or treated
 CC include hyperlipidaemia, cardiovascular disease, obesity, diabetes,
 CC cancer, neurological disorders and immunological disorders. DGAT may also
 CC be administered to males to increase sperm count. Also, transgenic plant

CC with altered levels of DGAT can be used to produce novel oils for
 CC consumption by humans, or for use as industrial feedstocks. Transgenic
 CC animals with altered levels of DGAT can be used as sources for a variety
 CC of different food and industrial products in which the triglyceride
 CC content is specifically tailored. The invention may enable development of
 CC anti-obesity, cardiant, cyrostatic or antilipemic compounds. The present
 CC sequence is that of the mouse DGAT protein of the invention. Note: The
 CC present sequence does not appear in the specification but was obtained by
 CC the index from GenBank.
 XX
 SQ Sequence 498 AA;
 Query Match 87.8%; Score 2278.5; DB 3; Length 498;
 Best Local Similarity 85.1%; Pred. No. 6-6e-239;
 Matches 421; Conservative 29; Mismatches 34; Indels 11; Gaps 3;
 QY 1 MGDR---GSSRRRTGSRPSSHGCGGPAABEYVDAAGDVGAGAPAPAP----- 51
 Db 1 MGDRCAGSSRRRRGSRVSVQGSQSGPYEEDVDAVSDLGAGGAPAPAPAPAPAPAP 60
 QY 52 NKDDGAGVSGHWEIQRRLDLSLSSSDSGFSNRYGILNWCVMWLTLSNARLPLENTIKY 111
 Db 61 DKDERTVGDGYMDRCHRLDLSLSSSDSGFSNRYGILNWCVMWLTLSNARLPLENTIKY 120
 QY 112 GILVDPIDVSLFLKDPHSPAPCLVTAANYFAVAAPQVBRRLAVGALTQAGLLAHVAN 171
 Db 121 GILVDPIDVSLFLKDPHSPAPCLVTAANYFAVAAPQVBRRLAVGALTQAGLLAHVAN 180
 QY 172 LATIICPPAAVVLVESTITPVGSLIAHMAHTILFKLFSTYDVNSWC--RRAPKAAGAG 229
 Db 181 LATIICPPAAVVALVESTITPVGSVFALASVIMFKLTSYDVNLMCRORVKAAGAVSTG 240
 QY 230 KKAASAAAPHVSPDNLTYRDLYVFLFAPLTCVLELNPSPRIKRFLLRIEMLEFT 289
 Db 241 KKVSGAAQAQVSPDNLTYRDLYVFLFAPLTCVLELNPSPRIKRFLLRIEMLEFT 300
 QY 290 QLOVGLIQMVPALIONSMKPKMDYSRIIERLKLAVPNHLIWLIFYYWLFHSCINAV 349
 Db 301 QLOVGLIQMVPALIONSMKPKMDYSRIIERLKLAVPNHLIWLIFYYWLFHSCINAV 360
 QY 350 AELMQFGDRBFYRDWMSSESTYTFQNNMTIVHKKCIRHFKYKMLRRGSSKMAARTGVFL 409
 Db 361 AELLQFGDRBFYRDWMSSESTYTFQNNMTIVHKKCIRHFKYKMLRRGSSKMAARTGVFL 420
 QY 410 ASAFHEVLVSPLMFRMLAFTGMAAQIPLAMFVGRFQGNVGNAAVWLSLIGQPIAV 469
 Db 421 TSAPFHEVLVSPLMFRMLAFTGMAAQIPLAMVIGRFRGNYGNAAVWLSLIGQPIAV 480
 QY 470 LMYVHDYVLTANTAPAA 484
 Db 481 LMYVHDYVLTANTAPAA 495
 RESULT 15
 ADS00390
 ID ADS00390 standard; protein; 498 AA.
 XX
 AC ADS00390;
 XX
 DT 16-DEC-2004 (first entry)
 DT
 XX Mouse diacylglycerol acyltransferase 1.
 DE
 XX Antiartherosclerotic; Antilipemic; Antidiabetic; Anorectic; Cardiant;
 KM diacylglycerol acyltransferase-1; glucose; cholesterol; triglyceride;
 KM lipid metabolism; cholesterol metabolism; atherosclerosis;
 KM hyperlipidaemia; diabetes; type 2 diabetes; obesity;
 KM cardiovascular disease; mouse; enzyme.
 OS Mus musculus.
 XX
 PN US2004185559-A1.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 5, 2006, 12:29:50 ; Search time 41 Seconds
(without alignments)
1145.214 Million cell updates/sec

Title: US-10-659-800-6
Perfect score: 2594
Sequence: 1 MCDRSSRRRTGSRPSSHG.....VMYVHDYVLYNEAPAAEA 488

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1106	42.6	496	2	probable sterol O-
2	791.5	30.5	520	2	diacylglycerol O-a
3	661	25.5	441	2	diacylglycerol O-a
4	467	18.0	231	2	sterol O-acyltrans
5	371	14.3	540	1	sterol O-acyltrans
6	345	13.3	550	1	sterol O-acyltrans
7	344.5	13.3	642	2	probable membrane
8	341.5	13.2	472	2	probable sterol O-
9	300	11.6	537	2	probable sterol O-
10	297	11.4	467	2	hypothetical prote
11	281.5	10.9	610	2	hypothetical prote
12	131.5	5.1	305	2	sterol O-acyltrans
13	121.5	4.7	560	2	probable membrane
14	117.5	4.5	452	2	sn-glycerol-3-phos
15	117.5	4.5	452	2	sn-glycerol-3-phos
16	116	4.4	609	2	probable membrane
17	113.5	4.4	452	1	glycerol-3-phospha
18	110	4.2	659	2	hypothetical prote
19	107.5	4.1	475	2	hypothetical prote
20	106.5	4.1	478	2	probable polyacch
21	106	4.1	495	2	probable alginat
22	106	4.1	527	2	probable alginat
23	100.5	3.9	478	2	alginate O-acetyla
24	99.5	3.8	567	2	menaquone biosyn
25	98.5	3.8	247	2	hypothetical prote
26	97	3.7	473	2	closely related to
27	96	3.7	267	1	corticotropin / 11
28	95.5	3.7	452	2	glycerol-3-phospha
29	95.5	3.7	519	2	tachykinin recepto

30	95.5	3.7	807	2	A34581	oxyterol-binding
31	95	3.7	426	2	UQ1459	Bcl protein precu
32	94.5	3.6	238	2	D70358	hydrogenase (EC 1.
33	94.5	3.6	457	2	T11283	NADH2 dehydrogenas
34	94.5	3.6	583	2	T11839	hypothetical prote
35	93	3.6	416	2	C65183	hypothetical 45.0
36	93	3.6	572	2	I39369	suvar(3)7 protein
37	93	3.6	932	2	S09151	alpha-1A-adrenergi
38	92.5	3.6	287	2	B75155	hypothetical prote
39	91.5	3.5	403	2	AF1536	Tetracycline resis
40	90.5	3.5	299	2	F75060	probable hydrogena
41	90.5	3.5	395	2	B96610	hypothetical prote
42	90.5	3.5	600	2	T11889	NADH2 dehydrogenas
43	90.5	3.5	1911	2	T43048	calcium channel al
44	90.5	3.5	2410	2	T43731	cell wall alpha-gl
45	90	3.5	659	2	T33557	hypothetical prote

ALIGNMENTS

RESULT 1
T19027
probable sterol O-acyltransferase (EC 2.3.1.26) H19N07.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 09-Jul-2004
C:Accession: T19027, T23106
R:Kerhaw, J.
submitted to the EMBL Data Library, June 1996
A:Reference number: T19061
A:Accession: T19027
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-496 <M1>
A:Cross-references: UNIPROT:Q45245; UNIPARC:UP1000007F625; EMBL:Z75526; PIDD:CAA9773.1
A:Experimental source: clone C06H2
R:Dobson, R.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19678
A:Accession: T23106
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-496 <M12>
A:Cross-references: UNIPARC:PI000007F625; EMBL:Z92835; PIDD:CA07399.1; GSPDB:GN00023;
A:Experimental source: clone H19N07
C:Genetics:
A:Gene: CESP:H19N07.4
A:Map position: 5
A:Introns: 5/3; 43/2; 77/3; 139/1; 171/3; 456/1
C:Superfamily: sterol O-acyltransferase
C:Keywords: acyltransferase; coenzyme A

Query Match 42.6%; Score 1106; DB 2; Length 496;
Best Local Similarity 43.7%; Pred. No. 2.2e-83;
Matches 220; Conservative 89; Mismatches 155; Indels 40; Gaps 6;

QY 6 SRRRRRTGSRPSSHGCGPAAAEVRRDAAGPDVGAAGDAAPAPNPDGAGVSGHME 65
DB 5 TGRRRR---QPSRTNSGLASSRR-----SSFAQNGNSRRKSSKMRGCE 46
QY 66 LRCHRLQDLSFSSDGSFNSYRGILNMCVMILTSNARLFLENLIRYGLIVDPQVVSJFL 125
DB 47 KVMHTAQDSLRSTSGMWNFRGFFRLSLDLVLSNGRVALENVIKXGILITPLQWISTFV 106
QY 126 KDPH--SWPAPCVIAANVPAVAAFQVEKRLAVGALTBOGLLIHVNLAITLCPAAV 182
DB 107 EHHYIWSGMPNIALILCNIIQLISVFGMEKILERSGMLNGFAAVYTSLVIAHLYIPVVV 166
QY 103 VLVVSEIIPVGSILALMAHTILFLKLFYRDVNSGCRARAPAAAGKKASAA----- 236
DB 167 TLTHKWKPLMSVVMGVIVALELFEIYSYGHNVWARRRRITELTKQVVDLAKKTDGP 226
QY 237 -----APHTVS--YPDNLTYRDLYYFLFAPTLCYEINFPSPRIKRFLRLTLE 284

Db 227 KQFMDLKOELSMHQAQAQYPAWLTLSNITYFMAAPLTCSEFFPRLLRKRKFLKRYE 286
Qy 285 MLFPTQLOVGLIQQMVPTIONSMPKMDYSRIERLLKLAVERNHLIWLFFTWLPHS 344
Db 287 LIFLSFLAALVQOQWVPVRNSMKPLSEMEYSRCLERLKLAIPNHLIWLFFYTFPHS 346
Qy 345 CLNAAVAELMOGDRREFYPMWNSSESVTFWQMNNTPVHKWCIRHFPKPLRBSSKMMAR 404
Db 347 FLNLIAELRLRFADREFFRPMFAETIGYFWSKNLPEVHFAVRAHYSPMKRNPSKMSAF 406
Qy 405 TGVFLASAFHFHYLVSPLRMFLMAFTGMAQIPLAWFGFRFFQ-GNYGNAVWLSLII 463
Db 407 FVVFVSANFHFHYLVSPLKIFRLMSYGMGOIPLSITTDKVRNGRGRTNIIVWLSLIV 466
Qy 464 GQPIAVLWYHDYVLYNVEAPAAE 487
Db 467 GQPLALMYGHDWYILNFGVSAVQ 490

RESULT 2

T52584
diacylglycerol O-acyltransferase (EC 2.3.1.20) [validated] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C.Accession: T52584
R.Hillis, M.J.; Lu, C.; Hobbs, D.H.
FEBS Lett. 452, 145-149, 1999
A.Title: Cloning of a cDNA encoding diacylglycerol acyltransferase from Arabidopsis thaliana
A.Reference number: 226127
A.Cross-references: UNIPROT:Q9SLD2; UNIPARC:UPI0000038437; EMBL:AJ131831; PTDN:CA844774.
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-520 <HL>
A.Cross-references: UNIPROT:Q9SLD2; UNIPARC:UPI0000038437; EMBL:AJ131831; PTDN:CA844774.
A.Experimental source: cultivar Columbia
C.Function:
A.Description: EC 2.3.1.20 [validated, MUID:99313150]; catalyzes the final acylation of
A.Pathway: triacylglycerol biosynthesis
C.Keywords: acyltransferase; coenzyme A

Query Match 30.5%; Score 791.5; DB 2; Length 520;
Best Local Similarity 38.0%; Pred. No. 2e-57;
Matches 194; Conservative 77; Mismatches 174; Indels 65; Gaps 17;
Qy 8 RRRRTGSRSSHG-----GPPAAEE-----VRDAAAPDVGAADAPA 48
Db 25 RLRRRKSRSDSNGLLSGSDNNSPSDDVGAADVDRIDSVVNDACG-TANLAGDNG 83
Qy 49 PAPNDGDAGVSGHWEIARC-----HRLDLSFSSDSGF-SNYRGILNMCVWL 96
Db 84 GGDNNGGRRGGEGEGNADATFTYRPSVAHRRARSPSSDAIFKSHAGLNFNCVVL 143
Qy 97 ILSNARLPLENLIKXGILV-DPIQVSLFLKDPHSPAPCLVIANVPAVAAFOVEKRLA 155
Db 144 IAVNRLIENLMKCGMLRTDFWFSRSLRD--WPLFMCCISISIFPLAAFTVEKVL 200
Qy 156 VQALTEQAGLLHVNLAITILCPRAAVLVLESITPVGSLMALMATIIFLKFYSR--- 212
Db 201 OKYISEPVVIFLHIIITMTBVLVPPVYVTLRCDASAFISGVTLMILT-CIYWLKLVSAHTS 259
Qy 213 -DVNSWCRBARAKAASAGKASAAAPHTVGYPDNLTYRDLVYFLPAPTLCEVLENPSPR 271
Db 260 YIIRS-----LANBAKAP-----EVSY--YSLKSLAYFWAPFLTCQPSYPRBA 304
Qy 272 RIRKFLRLRIEMLEFQTQLOVGLIQQMVPTIONSMPK-K-DMDYSRIERLLKLAVERN 330
Db 305 CIRKGVVAQPAKLIVFTGFMGFIIEQYINPIVRNSKHPKLGDLVYA--IERVLKLSVEN 362
Qy 331 HLIVLFFFWLHSCINAAVAELMOGDRREFYPMWNSSESVTFWQMNNTPVHKWCIRHY 390
Db 363 LVVWLCMPYCFPHLWNLIIAELLFCGDRBFYKDMWNAKSGVDYWRWNNMPVHKKMVRHLY 422

Qy 391 KPMRLRGSSKMMARTGVFLASAFHFHYLVSPLRMFLMAFTGMAQIPLAWFGFRFFQ 450
Db 423 FPCLRSKIPKTLAIIATLVSAVFHELCIAVPCRLFKMAFLGIMFQVPLV-FITNYIQE 481
Qy 451 NY-----GNAAVW-LSLIIIGQPIAVLWYHD 475
Db 482 RFGSTVGNMIFWFIQFICIQPWCVLVYHD 511

RESULT 3

H84576
diacylglycerol O-acyltransferase [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C.Accession: H84576
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MUID:20083487; PMID:10617197
A.Creation: H84576
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-441 <STO>
A.Cross-references: UNIPROT:Q9SLD2; UNIPARC:UPI000017A770; GB:AE002093; NID:G4191775; PI
A.Gene: At2g19450
A.Map position: 2

Query Match 25.5%; Score 661; DB 2; Length 441;
Best Local Similarity 34.3%; Pred. No. 9.7e-47;
Matches 173; Conservative 61; Mismatches 137; Indels 134; Gaps 17;

Qy 8 RRRRTGSRSSHG-----GPPAAEE-----VRDAAAPDVGAADAPA 48
Db 25 RLRRRKSRSDSNGLLSGSDNNSPSDDVGAADVDRIDSVVNDACG-TANLAGDNG 83
Qy 49 PAPNDGDAGVSGHWEIARC-----HRLDLSFSSDSGF-SNYRGILNMCVWL 96
Db 84 GGDNNGGRRGGEGEGNADATFTYRPSVAHRRARSPSSDAIFKSHAGLNFNCVVL 143
Qy 97 ILSNARLPLENLIKXGILV-DPIQVSLFLKDPHSPAPCLVIANVPAVAAFOVEKRLA 156
Db 144 IAVNRLIENLMK-----LDP-----VILKMDRCDASAF----- 173
Qy 157 GALTQAGLLHVNLAITILCPRAAVLVLESITPVGSLMALMATIIFLKFYSR--- 212
Db 174 -----LSGVTLMILT-----IWLKLVSAHTSY 198
Qy 213 DVNSWCRBARAKAASAGKASAAAPHTVGYPDNLTYRDLVYFLPAPTLCEVLENPSPR 272
Db 199 DIRS-----LANBAKAP-----EVSY--YSLKSLAYFWAPFLTCQPSYPRBA 243
Qy 273 IRKREFLRLRIEMLEFQTQLOVGLIQQMVPTIONSMPK-K-DMDYSRIERLLKLAVERN 331
Db 244 IRKGVVAQPAKLIVFTGFMGFIIEQYINPIVRNSKHPKLGDLVYA--IERVLKLSVEN 301
Qy 332 LILVLFPMWPHSCINAAVAELMOGDRREFYPMWNSSESVTFWQMNNTPVHKWCIRHY 391
Db 302 YVWLCMPYCFPHLWNLIIAELLFCGDRBFYKDMWNAKSGVDYWRWNNMPVHKKMVRHLY 361
Qy 392 PMLRRGSSKMMARTGVFLASAFHFHYLVSPLRMFLMAFTGMAQIPLAWFGFRFFQ 451
Db 362 PCLRSKIRKTLAIIATLVSAVFHELCIAVPCRLFKMAFLGIMFQV----- 408
Qy 452 YGNAAVW-LSLIIIGQPIAVLWYHD 475
Db 409 -GNMIFWFIQFICIQPWCVLVYHD 432

RESULT 4

T01294

sterol O-acetyltransferase homolog F27F23.26 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C:Accession: T01294
 R:Roundley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL Data Library, May 1998
 A:Description: Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence.
 A:Reference number: 214177
 A:Accession: T01294
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-231 <R0U>
 A:Cross-references: UNIPROT:Q9SDI2; UNIPARC:UPI000017B01B; EMBL:AC003058; NID:g1335250;
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Map position: 2
 A:Initrions: 44/3; 70/3; 104/3; 150/2; 177/3; 184/3; 205/3
 A:Note: F27F23.26

Query Match 18.0%; Score 467; DB 2; Length 231;
 Best Local Similarity 44.0%; Pred. No. 4.6e-31;
 Matches 103; Conservative 42; Mismatches 65; Indels 24; Gaps 8;

QY 193 GSLALMAHTILFLKLFYSYR---DVNSWCRBARAKASAGKASAAAPHTVSYPDNLT 248
 DB 11 GVTLMMLT-CIVMLKLVSYAHTSYDIRS-----LANAADKXNP-----EVSY--YYS 54

QY 249 YRDLYFLFAPPTLCYELNFPSPRIKRLRLILEMFLFTQLOGLIQOMNVPTIONSM 308
 DB 55 LKSLAYFVWAPPTLCQPSRSACIRKGVARQAFALVFTGFMETIIIOYINPIVRNKK 114

QY 309 KPEK-DMDYSRIERLKLAVPNHILMLIFPYMLFPHSCNAVAELMOFGDREPEYRDWNS 367
 DB 115 HPLKEDLYLA--TERVLKLSVENLYVLMCMFYCFHLMNIIILBELCFDQREFFYKDWMA 172

QY 368 ESVTYFMQNMNIPVHKMCIRHFYKPMRLRRGSSKMMARVGFLLASAFHE-YLVS 420
 DB 173 KSVGDYMRMMNIPVHKMVRHITYPCLRGSKIPKTLAIIIAFLVSAVFHEVILIS 226

RESULT 5

sterol O-acetyltransferase (EC 2.3.1.26) - mouse
 N:Alternate names: acyl-coenzyme A cholesterol acyltransferase
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: J49454; J04617
 R:Uelmen, P.J.; Oka, K.; Sullivan, M.C.; Chang, T.
 J. Biol. Chem. 270, 26192-26201, 1995
 A:Title: Molecular cloning of mouse ACAT.
 A:Reference number: 149454; MUID:96064687; PMID:7592824
 A:Accession: J49454
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-540 <RES>
 A:Cross-references: UNIPROT:061263; UNIPARC:UPI000002816F; GB:I42293; NID:g1066809; PIDN
 R:Green, S.; Steinhilber, D.; Quehenberger, O.
 Biochem. Biophys. Res. Commun. 218, 924-929, 1996
 A:Title: Cloning and expression in Xenopus oocytes of a mouse homologue of the human acy
 A:Reference number: J04617; MUID:96158986; PMID:8579615
 A:Accession: J04617
 A:Molecule type: mRNA
 A:Residues: 1-194, 'R', 196-540 <GRE>
 A:Cross-references: UNIPARC:PI0000170CD5; GB:S81092; NID:g1478335; PIDN:AAB36050.1; PID
 A:Experimental source: peritoneal macrophages
 C:Comment: This enzyme helps maintain cellular cholesterol homeostasis by catalyzing est
 y cholesterol and oxygenated sterols.
 C:Genetics:
 A:Gene: ACAT
 A:Map position: 1
 C:Superfamily: sterol O-acetyltransferase
 C:Keywords: acyltransferase; cholesterol; coenzyme A; endoplasmic reticulum; transmembr

Query Match 14.3%; Score 371; DB 1; Length 540;
 Best Local Similarity 27.1%; Pred. No. 1e-22;
 Matches 126; Conservative 70; Mismatches 167; Indels 102; Gaps 19;

QY 71 LQDSLPSSDSGSSNRGLMCCVVMIL-----SNARLFE-NLIRKGLIVDP 118
 DB 118 LDELFEVD---HRTTYHMFALILFLVSTIVDYIDEGRLVLEFLLVAFGKFT 173

QY 119 QY-----VSLFKDPHSWPAPCLVIAAVFAVAFOVERKRLVGLTEQGL 166
 DB 174 VITWVWAMFLSTLSIFPLFP-W-----AHGYSKSHPLIYSLV-----HGLL 216

QY 167 LHVAMLATILCPAAVVLVESITPVGSLALMAHTILFLKLSYRDVNSWCRBARAKA 226
 DB 217 FLVFLQGL-VLGFVPTVYVLAATLPASRLTILLEGRIIMK-----AHSFRENIPRL 269

QY 227 SAGKASGAADPTVSYPDNLTYYRLYFLFAPPTLCYELNFPSPRIKRLRLILEM- 285
 DB 270 NAAKSKSKDPLPTVN-----OYLFLFAPPTLIYRDNYRPTVVRGVAMQFLQVF 321

QY 286 --LFTQLOGLIQOMNVPTION-SMKPEKMDYSRIERLKLAV-----PNHILMLIF 337
 DB 322 GCLFVYVY--IFERLCAPLFNRIKQEP8-----ARVLVLCVNSILFGVILFUS 370

QY 338 FYMLFPHSCINAAVAELMOFGDREPEYRDWNSVTFMQNMNIPVHKMCIRHFYKPMRLRG 397
 DB 371 FPAFLHCHLMAFAEMLRKDRMFDYDWNSTSYNRYTNVVDMLYYVYKDLWLF 430

QY 398 SSKM--MARTGVFLASAFHEYLVPLR---MFLMAFTGMAQIPLANFGRFQ 450
 DB 431 SKRFKSAAMLAVFALSAVHVEYALALCLSYFVPLVFLFMFGM---AFNIVDSRRK 486

QY 451 NYGNAVMLSLIIGPIAVLMVVDHYV-----LNTAP 484
 DB 487 PWNIMVWASLPLGILICFTSGDEYARQHCPLNPTFLDYRP 531

RESULT 6

sterol O-acetyltransferase (EC 2.3.1.26) - human
 N:Alternate names: ACAT; acyl-coenzyme A cholesterol acyltransferase
 C:Species: Homo sapiens (man)
 C:Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 09-Jul-2004
 C:Accession: A59038; A48026
 R:Chang, C.C.Y.; Chang, T.Y.
 submitted to Genbank, May 1999
 A:Description: Molecular cloning and functional expression of human acyl-coenzyme A:cho
 A:Reference number: A59038
 A:Contents: correction
 A:Accession: A59038
 A:Molecule type: mRNA
 A:Residues: 1-550 <CH2>
 A:Cross-references: UNIPROT:P35610; UNIPARC:UPI0000135B5D; GB:I21934; NID:g4878021; PIDN
 R:Chang, C.C.Y.; Huh, H.Y.; Cadigan, K.M.; Chang, T.Y.
 J. Biol. Chem. 268, 20747-20755, 1993
 A:Title: Molecular cloning and functional expression of human acyl-coenzyme A:cholesterc
 A:Reference number: A48026; MUID:94012607; PMID:8407899
 A:Accession: A48026
 A:Molecule type: mRNA
 A:Residues: 1-206, 'R', 208-550 <CH2>
 A:Cross-references: UNIPARC:PI000014346C; GB:I21934
 C:Genetics:
 A:Gene: GDB:SOAT; STAT; ACAT
 A:Cross-references: GDB:251696; OMIM:102642
 A:Map position: 1q25-1q25
 C:Function:
 A:Description: catalyzes the esterification of cholesterol by acyl-CoA
 A:Pathway: cholesterol metabolism
 A:Note: helps maintain cellular cholesterol homeostasis; plays a role in the development
 C:Superfamily: sterol O-acetyltransferase
 C:Keywords: acyltransferase; cholesterol metabolism; coenzyme A; endoplasmic reticulum;
 F:409,491/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.3%; Score 345; DB 1; Length 550;
Best Local Similarity 26.8%; Pred. No. 1.4e-20;
Matches 121; Conservative 73; Mismatches 182; Indels 76; Gaps 19;

QY 71 LQDSIFSDSGFSNYRGLNMCVNLISNARLPLENTIKGILVDPQVVS-LFLKDP-128
DB 128 LDELLEVD---HIRTTHMFIALLILFISTLVVDYIDEGRLVLEFSLISYAGKPEPT-183
QY 129 --HSPACCLVIAAVFAVFAQVEKRLAVGALTQ-----AGLLHVNANLNTIICF-178
DB 184 VVMTW---WIMFISTFSVPYF-LFOHMYATGYSKSHPLIRSLFHFGLFMITQIG-VLGF-237
QY 179 PAAVVLVESITPYGSLALMAHTILFLKFSYRDVNSWCRPARAKAASAGKKAASAP-238
DB 238 GPTVVLAVLYLTPARAFI-----IIFGDIRVMAKHSVRNENVRVLNSAEKKS-----287
QY 239 HTVSYPDNLTYRDLVYFLPAPTLCYELNPPSPRIKRFLLRIIEML--PFTQLOVGLI-296
DB 288 -TVPIP--TVNQYLYFLFAPTLIYRDSYPRNPVTWVGVAKKFAQVGCFFYYVYI--F-341
QY 297 QQMWVPTIQN-SMKPFKMDYSRIIERLLKLAV-----PNHLIMLIFPYWLPHSCLNVA-350
DB 342 ERLCALPRLNKKQEPFS-----ARVAVLCVENSILPGVILFLTFPAFLHCWLNAP-393
QY 351 ELMQFDRBEFYRDWNSSESVTFYQNNWNI PVHAKCIRHFYKPMLRGSSKM--MARTGVF-408
DB 394 EMLRGDMFYKDMWNSTSYSYRYTANVVVDMLYYAKDFLWFFSRRFESAMLVAF-453
QY 409 LASAFHELYLVSPVLR---MFLMAFTGMAQIPLAMFVGRFQNGYGNAAVLSLI-463
DB 454 AVSAVAVHEYALAVCLSFYFVFLVFMFPGM---AFNFIYVDSRKKPIWNLMTWTSLEL-509
QY 464 GQPIAVLMVYHDYVY-----LNYEAR-484
DB 510 GNGVLLCFYSGEYARRHRCPLKNPTFLDYVR-541

RESULT 7
S63350
probable membrane protein YNR019w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein N3206
C/Species: Saccharomyces cerevisiae
C/Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C/Accession: S63350
R/Prohl, T.M.
submitted to the Protein Sequence Database, April 1996
A/Reference number: S63346
A/Accession: S63350
A/Molecule type: DNA
A/Residues: 1-642 <POH>
A/Cross-references: UNIPROT:P53629; UNIPARC:UPI0000125DBD; EMBL:Z71634; NID:g1302503; PI
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:ARE2
A/Cross-references: SGD:S0005302; MIPS:YNR019w
A/Map position: 14R
C/Superfamily: probable membrane protein YCR048w
C/Keywords: transmembrane protein #status predicted <TM1>
F/213-235/Domain: transmembrane #status predicted <TM2>
F/293-311/Domain: transmembrane #status predicted <TM3>
F/321-337/Domain: transmembrane #status predicted <TM4>
F/435-451/Domain: transmembrane #status predicted <TM5>
F/483-499/Domain: transmembrane #status predicted <TM6>
F/622-638/Domain: transmembrane #status predicted <TM6>

Query Match 13.3%; Score 344.5; DB 2; Length 642;
Best Local Similarity 28.6%; Pred. No. 1.9e-20;
Matches 98; Conservative 66; Mismatches 138; Indels 41; Gaps 13;

QY 159 LTEQGLLHVNANLTLCPRAAVLVV--SITVGSLLAMAHITLFLK--LFSYD-213
DB 311 LLEN---ILKHLWLSKIFLPHSLVLMLKMSHFAFYNGYLMGIEKLQPSKALAKYKDS-367

QY 214 VNSMCRBARAKAASAGKK-----ASSAAAPHVSYPDNLTYRDLVYFLFAFTLCYE-264
DB 368 IND-----PVIGALBKSCFCFSFELSQSLSDQTQGFPPNISAKSPFMFTMPTLIYQ-421
QY 265 LNFPSPIRKRFLLRLIEM--LFFQLOVGLIQQWVVTIQNSMKPFKMDYSRIE-321
DB 422 IEYPTKEIRSYVLEKICALFGTIFLMMIDAQIL--MYVANRAL-AVANSSEWTGLD-477
QY 322 RLKLKLA-----VPHNLI-WLIFPYWPHSCLNVAELMOGDRBEFYRDWNSSESVTFYF-374
DB 478 RLKLKGLLVIVGFIYMTYLDLIDALILNCVAELTRGDKYFYGDWNNCVSMADFS-537
QY 375 QNNWIPVHKWCIRHFY-KPMLRGSSSKWMAFGVPLASAFHELYLVSPVLRFLMAFTG-433
DB 538 RIMNIPVHKFLLRHVYHSSMSFPLKNSQATLMTFFLSSVHBLAMVYIFKRLRYLFF-597
QY 434 MMAQIPLAMFVGRFQGN---YGNAAVLSLIQPIAVLMVY-473
DB 598 QMLQMPVALVNTKFMNRRTIIGNVIFWLIGICMGPSVWCTLYL-640

RESULT 8
T41684
probable sterol o-acyltransferase 2 - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T41684
R/Wedder, H.; Dueserhoef, A.; McDougal, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1999
A/Reference number: Z21742
A/Accession: T41684
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-472 <MED>
A/Cross-references: UNIPROT:Q9U082; UNIPARC:UPI0000069EC3; EMBL:AL117183; PIDN:CA854864.
A/Experimental source: strain 972h-; clone pl pLE11
C/Genetics:
A/Gene: SPDB:SPCP1E11.05C
C/Superfamily: probable membrane protein YCR048w

Query Match 13.2%; Score 341.5; DB 2; Length 472;
Best Local Similarity 26.7%; Pred. No. 2.3e-20;
Matches 115; Conservative 73; Mismatches 173; Indels 69; Gaps 15;

QY 88 ILNMCVNLISNARLPLEN-----LIKY-GILVD---PIQVSLFLKDBHS-130
DB 66 VLFVVAASIMTFMS--FLENFELGRPVYGTIFKTFQSNLDDLAKADLMSMFL-----118
QY 131 WPAPCLVIAAVFAVFAQVEKRLAVGALTQAGLLHVNANLTLCPRAAVL--LVES-188
DB 119 -----LANPFQKIFALGYL-RWYGLGVLYSI-LILFLSHCVLRCLSN-161
QY 189 ITPVGSLLAMAHITLFLKFSYRDVNSW---CRPARAKAAS-----GKKAASAAAP-239
DB 162 WSWTRAMFILLHSMVILKHLKHSYNNVNGWYSYCVHSLKQSKTTDLDDDRSSVEFEH-221
QY 240 TV-----SYPDNLTYRDLVYFLPAPTLCYELNPPSPRIKRFLLRIIEMLFTQLOVG-294
DB 222 CLNHGNTYFENLITPNLDFLWPSLCYQLYYRTAHVRHLYLECALGTPGCTFLVY-281
QY 295 LIOQWVPTIQNSMKPFKDM--DYS-----RIERLLKLAVPNHLIWLIFPYWPHSCL-346
DB 282 ISDHMVVLAKAIRTIIEAPEDASATYFARLGHVTFAMFPWLSFLVFWYIFEGVC-341
QY 347 NAAVLEMOGDRBEFYRDWNSSESVTFYQNNWNI PVHAKCIRHFYKPMLRGSSSKMMATG-406
DB 342 NFSSEITFPARNFDDMMNCMTWDOFARTNKKRPVHYFLKLVVYV--LNSFWSKSLSTFF-400
QY 407 VFLASAFHELYLVSPVLRFLMAFTGMAQIPLAMFVGRFQGNV---GNAAVLSLI-463
DB 401 TFPVSSVHLVWGCTITLKINGYGLFQMTQIPIYIIOROKFVRRHRLGNAFNFSTII-460

RESULT 14

E91019

en-glycerol-3-phosphate permease (imported) - Escherichia coli (strain O157:H7, substrat

C/Species: Escherichia coli

C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C/Accession: E91019

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

Gawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc

A/Accession: E91019

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-452 <HAV>

A/Cross-references: UNIPROT:O8X5A0, UNIPARC:UPI00000D0CED, GB:BA000007, PIDN:BA036548.1,

A/Experimental source: strain O157:H7, substrain RMD 0509952

C/Genetics:

A:Superfamily: hexose phosphate transport protein unpt

Query Match 4.5%; Score 117.5; DB 2; Length 452;

Best Local Similarity 18.7%; Pred. No. 0.066;

Matches 68; Conservative 52; Mismatches 120; Indels 123; Gaps 17;

QY 143 PAVAAFOVE---KRLAVGALTEQ-----AGLLHVNALATILCFPAAVLVLESTIP 191

DB 67 FALSGISIAVGFSGKFMDSVSDRNPVFLPAGLIL-----AAAVMLFMGFVP 114

QY 192 VGSLLALMAHTILFLKLF-----SYRDVNSWCRRAPAKAASAGKASAAA- 237

DB 115 ----WATSSIAVMFVLFLFCGFMGMPGCGRTVHWMSQKERGIYSVWNCANVGSG 170

QY 238 -PHVSYDPNLTLYRDLVYFLFAPFLCYELNPPRSRIRKRLRLILEMFTQLQVGLI 296

DB 171 IPLLFLFGMAWFMNDMHAALYMPAFC-----AIVLALFAFAMMRDTP 212

QY 297 QOMWVPTIONSMPKMDYSRIIR-----LKLAVPNHLIWLIFPYMLFHSCLNAV 349

DB 213 QSCGLPTEBYKNDYDP--DYNEKAEOLTAQOIFMQYVLPNKLWYI-----AIVNVP 264

QY 350 AELMOFGDREFFYRDWMSSEVYTFWQNNNIPVHKWICIRHFYKPMRLRGSSKKMARTGVFL 409

DB 265 VYLLRYG---ILDM-----SPTYLKE-----VKNF-----ALDKSSW----- 293

QY 410 ASAFPHEYLVSVPFLMFLMAFTGMAOIPLAWFVGRFQGYGNAAVWLSLITIGOPNAV 469

DB 294 -AYFFEY-----AGIPGTLICGMSMDKVFGRNGRGTGVFFMTLV--TIAT 336

QY 470 LMY 472

DB 337 IVY 339

RESULT 15

G85863

en-glycerol-3-phosphate permease [imported] - Escherichia coli (strain O157:H7, substrat

C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C/Accession: G85863

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouets, K.; Apodaca,

Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A85480; MUID:21074935; PMID:11206551

A/Accession: G85863

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-452 <STO>

A/Cross-references: UNIPROT:O8X5A0, UNIPARC:UPI00000D0CED, GB:AE005174, NID:G12516580, F

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A:Gene: glpt

C:Superfamily: hexose phosphate transport protein unpt

Query Match 4.5%; Score 117.5; DB 2; Length 452;

Best Local Similarity 18.7%; Pred. No. 0.066;

Matches 68; Conservative 52; Mismatches 120; Indels 123; Gaps 17;

QY 143 PAVAAFOVE---KRLAVGALTEQ-----AGLLHVNALATILCFPAAVLVLESTIP 191

DB 67 FALSGISIAVGFSGKFMDSVSDRNPVFLPAGLIL-----AAAVMLFMGFVP 114

QY 192 VGSLLALMAHTILFLKLF-----SYRDVNSWCRRAPAKAASAGKASAAA- 237

DB 115 ----WATSSIAVMFVLFLFCGFMGMPGCGRTVHWMSQKERGIYSVWNCANVGSG 170

QY 238 -PHVSYDPNLTLYRDLVYFLFAPFLCYELNPPRSRIRKRLRLILEMFTQLQVGLI 296

DB 171 IPLLFLFGMAWFMNDMHAALYMPAFC-----AIVLALFAFAMMRDTP 212

QY 297 QOMWVPTIONSMPKMDYSRIIR-----LKLAVPNHLIWLIFPYMLFHSCLNAV 349

DB 213 QSCGLPTEBYKNDYDP--DYNEKAEOLTAQOIFMQYVLPNKLWYI-----AIVNVP 264

QY 350 AELMOFGDREFFYRDWMSSEVYTFWQNNNIPVHKWICIRHFYKPMRLRGSSKKMARTGVFL 409

DB 265 VYLLRYG---ILDM-----SPTYLKE-----VKNF-----ALDKSSW----- 293

QY 410 ASAFPHEYLVSVPFLMFLMAFTGMAOIPLAWFVGRFQGYGNAAVWLSLITIGOPNAV 469

DB 294 -AYFFEY-----AGIPGTLICGMSMDKVFGRNGRGTGVFFMTLV--TIAT 336

QY 470 LMY 472

DB 337 IVY 339

Search completed: May 5, 2006, 12:34:18

Job time : 43 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 5, 2006, 12:33:51 ; Search time 47 Seconds
(without alignments)
858.420 Million cell updates/sec

Title: US-10-659-800-6
Perfect score: 2594
Sequence: 1 MGDGSSRRRTGSRPSHG.....VLMYVHDYVLYNEAPAAEA 488

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2594	100.0	488	2	US-09-165-042-1 Sequence 1, Appl1
2	2299.5	88.6	500	2	US-09-326-203A-17 Sequence 17, Appl1
3	2278.5	87.8	498	2	US-09-899-645A-8 Sequence 8, Appl1
4	2273.5	87.6	498	2	US-09-103-754A-5 Sequence 5, Appl1
5	2039	78.6	386	2	US-09-103-754A-4 Sequence 4, Appl1
6	1106	42.6	496	2	US-09-326-203A-18 Sequence 18, Appl1
7	791.5	30.5	520	2	US-09-326-203A-2 Sequence 2, Appl1
8	779.5	30.1	503	2	US-09-593-359-4 Sequence 4, Appl1
9	656.5	25.3	341	2	US-09-593-359-2 Sequence 2, Appl1
10	551	21.2	163	2	US-09-774-639-230 Sequence 230, App
11	431	16.6	75	2	US-09-774-639-125 Sequence 125, App
12	375.5	14.5	522	2	US-09-165-042-3 Sequence 3, Appl1
13	375.5	14.5	522	2	US-09-949-016-11030 Sequence 11030, A
14	370.5	14.3	502	2	US-09-326-203A-23 Sequence 23, Appl1
15	367.5	14.2	502	2	US-09-328-857A-4 Sequence 4, Appl1
16	343.5	13.2	525	2	US-09-328-857A-3 Sequence 3, Appl1
17	343	13.2	550	1	US-08-121-057-4 Sequence 4, Appl1
18	343	13.2	550	1	US-08-509-187D-4 Sequence 4, Appl1
19	343	13.2	550	4	US-09-121-396-4 Sequence 4, Appl1
20	343	13.2	550	4	PCR-US93-09704A-4 Sequence 4, Appl1
21	337	13.0	60	2	US-09-774-639-237 Sequence 237, App
22	336.5	13.0	432	2	US-09-326-203A-35 Sequence 35, Appl1
23	312	12.0	51	2	US-09-165-042-9 Sequence 9, Appl1
24	281.5	10.9	429	2	US-09-326-203A-24 Sequence 24, Appl1
25	281.5	10.9	610	2	US-09-709-457-2 Sequence 2, Appl1
26	275.5	10.6	419	2	US-09-248-796A-17982 Sequence 17982, A
27	259	10.0	48	2	US-09-774-639-238 Sequence 238, App

28	255	9.8	47	2	US-09-774-639-239	Sequence 239, App
29	145	5.6	53	2	US-09-165-042-8	Sequence 8, Appl1
30	142	5.5	53	2	US-09-165-042-7	Sequence 7, Appl1
31	137	5.3	52	2	US-09-165-042-6	Sequence 6, Appl1
32	134	5.2	2	2	US-09-774-639-235	Sequence 235, App
33	132	5.1	26	2	US-09-165-042-5	Sequence 5, Appl1
34	118	4.5	18	2	US-09-774-639-236	Sequence 236, App
35	112	4.3	30	2	US-09-165-042-17	Sequence 17, Appl1
36	111	4.3	250	2	US-09-326-203A-22	Sequence 22, Appl1
37	109.5	4.2	409	2	US-09-248-796A-14863	Sequence 14863, A
38	106.5	4.1	33	2	US-09-165-042-10	Sequence 10, Appl1
39	103.5	4.0	457	2	US-09-489-039A-8293	Sequence 8293, Ap
40	103	4.0	343	2	US-09-489-039A-9368	Sequence 9368, Ap
41	101.5	3.9	432	2	US-09-255-368-2	Sequence 2, Appl1
42	101.5	3.9	432	2	US-09-405-558-2	Sequence 2, Appl1
43	101.5	3.9	432	2	US-09-538-036-2	Sequence 2, Appl1
44	101	3.9	576	2	US-09-540-236-2286	Sequence 2286, Ap
45	100.5	3.9	487	2	US-09-790-838-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1									
US-09-165-042-1									
; Sequence 1, Application US/09165042									
; Patent No. 6100077									
; GENERAL INFORMATION:									
; APPLICANT: Sturley, Stephen L.									
; APPLICANT: Oelkers, Peter									
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL									
; FILE REFERENCE: 0575/56331									
; CURRENT APPLICATION NUMBER: US/09/165,042									
; CURRENT FILING DATE: 1998-10-01									
; NUMBER OF SEQ ID NOS: 32									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO 1									
; LENGTH: 488									
; TYPE: PRT									
; ORGANISM: Yeast									
US-09-165-042-1									
Query Match									
Beet Local Similarity 100.0%; Pred. No. 1.6e-255; Length 488;									
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MGDRSSRRRTGSRPSHG	GGGPAABE	EV	RDAA	AG	PDVGA	AD	PAPAPKDGAGVG 60
DB	1	MGDRSSRRRTGSRPSHG	GGGPAABE	EV	RDAA	AG	PDVGA	AD	PAPAPKDGAGVG 60
QY	61	SGHWEI	LRCH	RODS	IFSS	DSG	FSN	RGIL	WCVMLISNARLFLENIKYGIIVDPYQV 120
DB	61	SGHWEI	LRCH	RODS	IFSS	DSG	FSN	RGIL	WCVMLISNARLFLENIKYGIIVDPYQV 120
QY	121	VSLF	KDHP	AP	CLV	IA	AV	FA	VAARQVEKRLAVGALT
DB	121	VSLF	KDHP	AP	CLV	IA	AV	FA	VAARQVEKRLAVGALT
QY	181	AVVL	LVES	IT	VG	SL	AL	MA	HTILFLKLF
DB	181	AVVL	LVES	IT	VG	SL	AL	MA	HTILFLKLF
QY	241	VSY	PNL	TY	R	LY	FL	P	PTCYELANFRB
DB	241	VSY	PNL	TY	R	LY	FL	P	PTCYELANFRB
QY	301	VPT	ION	SK	MP	R	D	Y	SRIRERFLRLILEML
DB	301	VPT	ION	SK	MP	R	D	Y	SRIRERFLRLILEML
QY	361	YR	D	W	N	S	E	S	VYTFWQNMNIPVHK
DB	361	YR	D	W	N	S	E	S	VYTFWQNMNIPVHK

Db 361 YRDWNNSESVTYFMQNNWNPVHKWCI RHFYKEMLRGSSKMMARIGVFLASAFHEYLVS 420
QY 421 VPLRMFLMAFTGMMAOIPLAMFVGRFGCGNYGNAVMWLSLIIIGPIATLMTVHDYVLAN 480
Db 421 VPLRMFLMAFTGMMAOIPLAMFVGRFGCGNYGNAVMWLSLIIIGPIATLMTVHDYVLAN 480
QY 481 YEAPAAEA 488
Db 481 YEAPAAEA 488

RESULT 2
US-09-326-203A-17
; Sequence 17, Application US/09326203A
; Patent No. 6444876

; GENERAL INFORMATION:
; APPLICANT: Laesener, Mike
; APPLICANT: Ruzelnsky, Diane
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; FILE REFERENCE: 17045/00/WO
; CURRENT APPLICATION NUMBER: US/09/326,203A
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-326-203A-17

Query Match 88.6%; Score 2299.5; DB 2; Length 500;
Best Local Similarity 85.9%; Pred. No. 1.8e-225;
Matches 427; Conservative 26; Mismatches 31; Indels 13; Gaps 3;

QY 1 MGRD---GSSRRRTGSRPSSHGCGGPAABEEVDAAAGDPVGAADAPAPAP----- 51
Db 1 MGRDGAAGSSRRRTGSRPSSHGCGGPAABEEVDAAAGDPVGAADAPAPAPAPAH 60
QY 52 --NKGDGAGVSGHWECHRLODSLFSDSGFSNYRGILNMCVWLILSNARLFLENL 109
Db 61 TRDKORQSVGSGHWECHRLODSLFSDSGFSNYRGILNMCVWLILSNARLFLENL 120
QY 110 KYGIIIVDPIQVVSFLKDPHSPAPCLVIANVFAVAAFQVEKRLAVGALTQAGLLHY 169
Db 121 KYGIIIVDPIQVVSFLKDPHSPAPCLVIANVFAVAAFQVEKRLAVGALTQAGLLHY 180
QY 170 ANLATIICPPAAVVLVVESTIPVGSLLMAHTIIFLKFSYRDVNSWC--RRARAKAS 227
Db 181 VNLATITICPPAAVVLVVESTIPVGSLLMAHTIIFLKFSYRDVNSWC--RRARAKAS 240
QY 228 AGKASAAAPHVTSYPDNLTYRDLYFLFAPTLCYELNFPSPRIKRFLLRRIEMLF 287
Db 241 AGKVSAAAPHVTSYPDNLTYRDLYFLFAPTLCYELNFPSPRIKRFLLRRIEMLF 300
QY 288 FTQLOVGLIQOMVPTIONSMPKPKMDYSRIIEBLLKLAVDNHLIWLIFFYWLFHSCIN 347
Db 301 FTQLOVGLIQOMVPTIONSMPKPKMDYSRIIEBLLKLAVDNHLIWLIFFYWLFHSCIN 360
QY 348 AVALMOGDFREYVDWNNSESVTYFMQNNWNPVHKWCI RHFYKEMLRGSSKMMARIGV 407
Db 361 AVALMOGDFREYVDWNNSESVTYFMQNNWNPVHKWCI RHFYKEMLRGSSKMMARIGV 420
QY 408 FLASAFHEYLVS VPLRMFLMAFTGMMAOIPLAMFVGRFGCGNYGNAVMWLSLIIIGPI 467
Db 421 FLASAFHEYLVS VPLRMFLMAFTGMMAOIPLAMFVGRFGCGNYGNAVMWLSLIIIGPI 480
QY 468 AVLMTVHDYVLAN YEAP 484
Db 468 AVLMTVHDYVLAN YEAP 484

Db 481 AVLMTVHDYVLAN YEAP 497

RESULT 3
US-09-899-645A-8
; Sequence 8, Application US/09899645A
; Patent No. 6914170

; GENERAL INFORMATION:
; APPLICANT: Li, Chun Ping
; APPLICANT: Zheng, Peizhong
; APPLICANT: Nicholas, Scott
; TITLE OF INVENTION: METHODS FOR REGULATING BETA-OXIDATION IN PLANTS
; FILE REFERENCE: 35718/235742
; CURRENT APPLICATION NUMBER: US/09/899,645A
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/216,211
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-899-645A-8

Query Match 87.8%; Score 2278.5; DB 2; Length 498;
Best Local Similarity 85.1%; Pred. No. 2.4e-223;
Matches 421; Conservative 29; Mismatches 34; Indels 11; Gaps 3;

QY 1 MGRD---GSSRRRTGSRPSSHGCGGPAABEEVDAAAGDPVGAADAPAPAP----- 51
Db 1 MGRDGAAGSSRRRTGSRPSSHGCGGPAABEEVDAAAGDPVGAADAPAPAPAHTR 60
QY 52 NKGDGAGVSGHWECHRLODSLFSDSGFSNYRGILNMCVWLILSNARLFLENL 111
Db 61 DKDGRTVGDGWDRCRLODSLFSDSGFSNYRGILNMCVWLILSNARLFLENL 120
QY 112 GILVDPLOVVSFLKDPHSPAPCLVIANVFAVAAFQVEKRLAVGALTQAGLLHYAN 171
Db 121 GILVDPLOVVSFLKDPHSPAPCLVIANVFAVAAFQVEKRLAVGALTQAGLLHYAN 180
QY 172 LATIICPPAAVVLVVESTIPVGSLLMAHTIIFLKFSYRDVNSWC--RRARAKASAG 229
Db 181 LATIICPPAAVVLVVESTIPVGSLLMAHTIIFLKFSYRDVNSWC--RRARAKASAG 240
QY 230 KASAAAPHVTSYPDNLTYRDLYFLFAPTLCYELNFPSPRIKRFLLRRIEMLF 289
Db 241 KVSAAAPHVTSYPDNLTYRDLYFLFAPTLCYELNFPSPRIKRFLLRRIEMLF 300
QY 290 QLOVGLIQOMVPTIONSMPKPKMDYSRIIEBLLKLAVDNHLIWLIFFYWLFHSCINAV 349
Db 301 QLOVGLIQOMVPTIONSMPKPKMDYSRIIEBLLKLAVDNHLIWLIFFYWLFHSCINAV 360
QY 350 AELMOGDFREYVDWNNSESVTYFMQNNWNPVHKWCI RHFYKEMLRGSSKMMARIGV 409
Db 361 AELMOGDFREYVDWNNSESVTYFMQNNWNPVHKWCI RHFYKEMLRGSSKMMARIGV 420
QY 410 ASAFHEYLVS VPLRMFLMAFTGMMAOIPLAMFVGRFGCGNYGNAVMWLSLIIIGPIAV 469
Db 421 TSAPHEYLVS VPLRMFLMAFTGMMAOIPLAMFVGRFGCGNYGNAVMWLSLIIIGPIAV 480
QY 470 LMTVHDYVLAN YEAP 484
Db 481 LMTVHDYVLAN YEAP 495

RESULT 4
US-09-103-754A-5
; Sequence 5, Application US/09103754A
; Patent No. 6344548
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert
; APPLICANT: Cassee, Sylvaine

APPLICANT: Smith, Steven
APPLICANT: Erickson, Sandra
TITLE OF INVENTION: Diacylglycerol O-acyltran
TITLE OF INVENTION: sfetase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Bozicevic & Reed
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,754A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 6510-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650 327 3400
TELEFAX: 650 327 3231
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-103-754A-5

Query Match 87.6%; Score 2273.5; DB 2; Length 498;
Best Local Similarity 84.8%; Pred. No. 7.8e-223;
Matches 420; Conservative 29; Mismatches 35; Indels 11; Gaps 3;
QY 1 MGR---GSSRRRRGSSRRSSSHGGGPPAAEEVDAAAGPVGAAGDAPAP----- 51
DB 1 MGRGAGSSRRRRGSSRRSSSHGGGPPAAEEVDAAAGPVGAAGDAPAPAHTR 60
QY 52 NKDAGAGVSGHWEIACHRLDLSLSSDSGFSNNGIIMWCVMILISNARFLENLKY 111
DB 61 DKDGTSGVGDWDKCHRLDLSLSSDSGFSNNGIIMWCVMILISNARFLENLKY 120
QY 112 GILVDPIDVNSLFLKDPHSPWAPCLVIANVFAVAFOVEKRLAVGALTQAGLLHYAN 171
DB 121 GILVDPIDVNSLFLKDPHSPWAPCLVIANVFAVAFOVEKRLAVGALTQAGLLHYAN 180
QY 172 LATILCFPAAVVLLVESITPVGSLIALMAHTILFLKLFPSYRDVNSWC--RRARAPASAG 229
DB 181 LATILCFPAAVVLLVESITPVGSLIALMAHTILFLKLFPSYRDVNSWC--RRARAPASAG 240
QY 230 KKASAAAPHVTSYDNLTYRDLVYFLFAPLTCYELNPPRSPIRKRFILRLILMLPPT 289
DB 241 KKVSAAQAQVAVSYDNLTYRDLVYFLFAPLTCYELNPPRSPIRKRFILRLILMLPPT 300
QY 290 QLVGLIQOMWVPTIIONSMKPKMDYSRIERLKLAVPNHLIMLIFPYWLFHSCLANV 349
DB 301 QLVGLIQOMWVPTIIONSMKPKMDYSRIERLKLAVPNHLIMLIFPYWLFHSCLANV 360
QY 350 AELMOPGREFRDMWNSSEVTFWQNNNIPYHKACIRHFYPMIRGSSKMMATGVPFL 409
DB 361 AELMOPGREFRDMWNSSEVTFWQNNNIPYHKACIRHFYPMIRGSSKMMATGVPFL 420

QY 410 ASAFHEYLVSVPRLMAFTGMAAOIPLAMFYGRFQGNYGNAAVLSLIGQPIAV 469
DB 421 TSAPFHEILVSVPRLMAFTGMAAOIPLAMFYGRFQGNYGNAAVLSLIGQPIAV 480
QY 470 LMYVDYVLYNYP 484
DB 481 LMYVDYVLYNYP 495

RESULT 5
US-09-103-754A-4
Sequence 4, Application US/09103754A
Patent No. 6344548
GENERAL INFORMATION:
APPLICANT: Farese, Robert
APPLICANT: Cases, Sylvaine
APPLICANT: Smith, Steven
APPLICANT: Erickson, Sandra
TITLE OF INVENTION: Diacylglycerol O-acyltran
TITLE OF INVENTION: sfetase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Bozicevic & Reed
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,754A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 6510-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650 327 3400
TELEFAX: 650 327 3231
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-103-754A-4

Query Match 78.6%; Score 2039; DB 2; Length 386;
Best Local Similarity 99.5%; Pred. No. 4.3e-199;
Matches 384; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 103 LFLNLIRYGLVNPIDVNSLFLKDPHSPWAPCLVIANVFAVAFOVEKRLAVGALTQ 162
DB 1 LFLNLIRYGLVNPIDVNSLFLKDPHSPWAPCLVIANVFAVAFOVEKRLAVGALTQ 60
QY 163 AGLLHVANLNTILCFPAAVVLLVESITPVGSLIALMAHTILFLKLFPSYRDVNSWCRRAR 222
DB 61 AGLLHVANLNTILCFPAAVVLLVESITPVGSLIALMAHTILFLKLFPSYRDVNSWCRRAR 120
QY 223 AKASAGKASSAAAPHVTSYDNLTYRDLVYFLFAPLTCYELNPPRSPIRKRFILRLI 282
DB 121 AKASAGKASSAAAPHVTSYDNLTYRDLVYFLFAPLTCYELNPPRSPIRKRFILRLI 180

QY 283 LEMHFFTOLOVGLIOQMNVPTIONSMPKDKMDYSRIIERLKLAVPNHLIWLIFFWLF 342
DB 181 LEMHFFTOLOVGLIOQMNVPTIONSMPKDKMDYSRIIERLKLAVPNHLIWLIFFWLF 240
QY 343 HSCINAAVELMOFGDREYRDWMNSESVTYFWQNNIPVHKCIRHFKKIPMLRRSSKMM 402
DB 241 HSCINAAVELMOFGDREYRDWMNSESVTYFWQNNIPVHKCIRHFKKIPMLRRSSKMM 300
QY 403 ARTGVFLASAFHEHYLVSVPLRMFLMAFTGMAQIPLAMFVGFPQNGYNAAVMLSLI 462
DB 301 ARTGVFLASAFHEHYLVSVPLRMFLMAFTGMAQIPLAMFVGFPQNGYNAAVMLSLI 360
QY 463 IGOPIAVLMYVHDYVLYVLYEAPAAEA 488
DB 361 IGOPIAVLMYVHDYVLYVLYEAPAAEA 386

RESULT 6
US-09-326-203A-18
Sequence 18, Application US/09326203A
Patent No. 6444876
GENERAL INFORMATION:
APPLICANT: Laesener, Mike
APPLICANT: Ruzinskiy, Diane
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
FILE REFERENCE: 17045/00/WO
CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 496
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-326-203A-18

Query Match 42.6%; Score 1106; DB 2; Length 496;
Best Local Similarity 43.7%; Pred. No. 7,8e-104;
Matches 220; Conservative 89; Mismatches 155; Indels 40; Gaps 6;
QY 6 SRRRTGSRPSHSGCGGAPAAAEERDAAGDPVGAAGDAPAPAPNDGAGVSGSME 65
DB 5 TGRRRR---QPSRTSNGSLASSRR-----SSFAQNGNSSRKSSEKRGFCE 46
QY 66 LRCHRLQDLSFSSDSGFNRYGILNMCVMLILSNARLFLENTLIRYGLIIVDPPIQVLSFL 125
DB 47 KVVHTAQDSLSFTSGMTNFRGFPLSLILLVLSNGRALEEVIRKXGILITPLQWISIFV 106
QY 126 KDPH--SWAPCLVIANVPAVAAFOVEKRLAVALTEQAGLLIHAVNLATILCFPAV 182
DB 107 EHHYSIMSPMLATILGNITQLSVFGMEKILIERGMLNGFAAVFTSLVIMHTIPVV 166
QY 183 VLAVESITPVGSLALMAHTILFLKPSYRDVNSCRBARAKAAGKASSA----- 236
DB 167 TLTHKMKPLWSVVMGVVIEALKFISYGHVNYARDRRKITLKTQVTDLAKKTD 226
QY 237 -----APHTVS--YPDNLTYRDLYFLAFAPTLCEYELNFPSPRIKRFLRLRIE 284
DB 227 KQPMOLKDELSMHQAAQYPAVLTLSNIYFPAATLICEFEPFLRLIRKHFILKRTYE 286
QY 285 MLFTQLOVGLIOQMNVPTIONSMPKDKMDYSRIIERLKLAVPNHLIWLIFFWLFS 344
DB 287 LIFLSFLIAALVQGVVVPTRNSMKPLSEMEYSRCLEERLLKLAIPNHLIWLIFFTFHS 346
QY 345 CLNAAELMORGDFEYRDWMNSESVTYFWQNNIPVHKCIRHFKKIPMLRRSSKMMAR 404
DB 347 FLNLIAELLRADREFYRDWMNSESVTYFWQNNIPVHKCIRHFKKIPMLRRSSKMMAR 406

QY 405 TGVFLASAFHEHYLVSVPLRMFLMAFTGMAQIPLAMFVGFRFO-GNYNAAVMLSLI 463
DB 407 FVFEVSAFHEHYLVSVPLKIFRLMSYGMWGQIPLSITDKVVRGRTGNIIVLSLIV 466
QY 464 GQPIAVLMYVHDYVLYVLYEAPAAE 487
DB 467 GQPIAVLMYVHDYVLYVLYEAPAAE 490

RESULT 7
US-09-326-203A-2
Sequence 2, Application US/09326203A
Patent No. 6444876
GENERAL INFORMATION:
APPLICANT: Laesener, Mike
APPLICANT: Ruzinskiy, Diane
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
FILE REFERENCE: 17045/00/WO
CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 520
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-326-203A-2

Query Match 30.5%; Score 791.5; DB 2; Length 520;
Best Local Similarity 38.0%; Pred. No. 9,5e-72;
Matches 194; Conservative 77; Mismatches 174; Indels 65; Gaps 17;
QY 8 RRRRTGSRPSHSGCGGAPAAAEERDAAGDPVGAAGDAPAPAPNDGAGVSGSME 48
DB 25 RLRRKRSRSDSSNGLLSGDNNSPSDVGAFAVDVRIDSVVDDAQG-TANLAGDNG 83
QY 49 PAPNKDAGVSGSHWEIARC-----HRLQDLSFSSDSGF-SYRILNMCVML 96
DB 84 GDDNNGGGRGGEGRGADATFYRPSVPAHRRARESPSSDAIFKSHAGLFNLGVVL 143
QY 97 ILSNARLFLENTLIRYGLIIV-DPIQVLSFLKDPHSMWAPCLVIANVPAVAAFOVEKRLA 155
DB 144 IAVNSRLIENLMKYLIRDFWPSRSRLD---WPLFPCICLSIFPLAFTVEKVL 200
QY 156 VQALTEQAGLLIHAVNLATILCFPAVVLVLESITPVGSLALMAHTILFLKFSYR-- 212
DB 201 QKYSIEPVILHIIITWTEVLVYVYTLRCDSAFLSGVTMLLT-CIVMLKVSATHS 259
QY 213 -DVNSWCRBARAKAASAKKASSAAAPHTYSYPDNLTYRDLYFLAFAPTLCEYELNFPSP 271
DB 260 YDIRS-----LANADKAMP-----EVSY--YVSLKSLAYPMVAVTLCYQSPSPSA 304
QY 272 RIRKRFILRLILEMLFTQLOVGLIOQMNVPTIONSMPKDKMDYSRIIERLKLAVPN 330
DB 305 CIRKGMVARQPAKIVIFGFGFIIEQYINIVANSKPLKGDLLXA--IRVILKLSVFN 362
QY 331 HLIMLIFFWLFSHCLNAAVELMOFGDREYRDWMNSESVTYFWQNNIPVHKCIRHFK 390
DB 363 LYYVLMCFYCFHLMINILAEILCFGDFEFKDMWNKASVGDYRMNMMPVHKMVRHLY 422
QY 391 KPMILRGSSKMMATGVFLASAFHEHYLVSVPLRMFLMAFTGMAQIPLAMFVGFRFOG 450
DB 423 FPCILRSKIPKTIATIIIFLVSVAVHELICIAVPCRLFKLMAFLGIMFOVPLV-FTTNYLOB 481
QY 451 NY-----GNAAVN-LSLIIGOPIAVLMYVHD 475
DB 482 RFGSTVGMMITWFIPLFPGDPMCVLLIYHD 511

```
RESULT 8
US-09-593-359-4
; Sequence 4, Application US/09593359
; Patent No. 6552250
; GENERAL INFORMATION:
; APPLICANT: Laroche, Andre J.
; APPLICANT: Nykiforuk, Cory L.
; APPLICANT: Weselake, Randall J.
; TITLE OF INVENTION: Diacylglycerol O-acyltransferase
; FILE REFERENCE: 24015U50
; CURRENT APPLICATION NUMBER: US/09/593,359
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Brassica napus
; OTHER INFORMATION: DGAT1
US-09-593-359-4
```

```
Query Match          30.1%; Score 779.5; DB 2; Length 503;
Best Local Similarity 38.7%; Pred. No. 1.5e-70;
Matches 191; Conservative 83; Mismatches 168; Indels 51; Gaps 15;
```

```
QY 10 RRTGSRPSHG-----GGGPAABEEVDAAGPDV--GAADDAAPAPAKXGDDGV 59
DB 26 RKKSSDSSNGLLSPTSPSDVGAABAEEDRVDAABEBAOCTANLAGDADRESAGG- 84
QY 60 GSGHWELRC-----HRLQDSLFSSDSGCF-SNYRGILNWCVMILISNARLFLENLI 109
DB 85 -----DVAFTYRSPVAHRRTRRESPLSSDAIFKSHAGLFNLCYVVLVAVNSRLIENIM 139
QY 110 KYGILV-DPIQVVSJFLKDPHWPAPCLVIANVFAVAFOVEKCLAVGALTQOAGLLH 168
DB 140 KYGWLIRDFWFSSTSLRD---WPLFMCLSLSVPLAFTVEKAVLQKFISEPAVAILH 196
QY 169 VANLATICPPAAVVLVESTITPVGSLALMAHTLFLKLFYRYVNSMCRABAKASA 228
DB 197 VITMTVLPYVYVTLRCDASFLSGVTMLLT-CIVMLKLVSAHTS--YDIRFLANSA 252
QY 229 GKKASSAAPHVTSYDNLTYRDLTYFLFAPTLCEYLNFPSPRIKRFLLRILEMLF 288
DB 253 DK-----VDPEISY--YVSLKSLAYFMVAAPTLCQPSYPSPCIRKGMVARQLAKYIF 304
QY 289 TQLOVGLIQQWNPPTIQNSMKPFK-DMDYSRIIEELKLAVPNHLIWLIFYYWLFHSCIN 347
DB 305 TGLMGFIIEQYINPIVRNSKHPLKGDLLYA--IERVLKLSVPLVYVWLCMFYCFHLMIN 362
QY 348 AVALMORGDEEFYRDMNNSSEVYTFMQNNMIPVHKMCIHFYKMKMLRGSSKMMARCTGV 407
DB 363 TLABELCGDEEFYKDMNNAKSVGDYWRMNMNPAHKMVRHAYFFCLIKIKPKVPAIIIA 422
QY 408 FLASAFHEHYVSVPLRMFRILMAFTGMMAOIPLAFVGRFGQNGNAAVWL-----SLI 462
DB 423 FLVGAFFHELCIAVDCRFLNMAFWGIMFQVPLV-FITNFIQERFGSNVGNMIRBSASCI 481
QY 463 IGPPIAVLMVYVD 475
DB 482 FGQPMWCGLLYYHD 494
```

```
RESULT 9
US-09-593-359-2
; Sequence 2, Application US/09593359
; Patent No. 6552250
; GENERAL INFORMATION:
; APPLICANT: Laroche, Andre J.
; APPLICANT: Nykiforuk, Cory L.
; APPLICANT: Weselake, Randall J.
; TITLE OF INVENTION: Diacylglycerol O-acyltransferase
; FILE REFERENCE: 24015U50
```

```
; CURRENT APPLICATION NUMBER: US/09/593,359
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Brassica napus
; OTHER INFORMATION: DGAT2
US-09-593-359-2
```

```
Query Match          25.3%; Score 656.5; DB 2; Length 341;
Best Local Similarity 41.9%; Pred. No. 3e-58;
Matches 144; Conservative 62; Mismatches 117; Indels 21; Gaps 8;
```

```
QY 138 IAAVFAVAFOVEKCLAVGALTQOAGLLHYANLATICPPAAVVLVESTITPVGSLIA 197
DB 4 LLSIFPLAFAFVEELVLOKCISEBVIFLHYITMTVLPVYVTLRCDASFLLSGDTLM 63
QY 198 LMAHTILFLKLFESYRDVNSMCRABAKASAGKASAAAPHVTSYDNLTYRDLTYFLF 257
DB 64 LIT-CIVMLKLVSAHTYDIR-----TLANSDDKAMP-----EVSY--YVSLKSLAYFNL 111
QY 258 APTLCYELNFPSPRIKRFLLRILEMLFTQLOVGLIQQWNPPTIQNSMKPFK-DMDY 316
DB 112 APTLCYQPSYRSPCIRKGMVARQPAKLVITGLMGFIIEQYINPIVRNSKHPLKGDLLY 171
QY 317 SRIIRLKLAVPNHLIWLIFYYWLFHSCLNAAVAELMOPGDEFRYRDMNNSSEVYFMQN 376
DB 172 A--IERVLKLSVPLVYVWLCMFYCFHLMINILAEILCFGDEEFYKDMNNAKSVGDYWRM 229
QY 377 WNIPIHKACIRHFYKPMRLRGSSKMMARCTGVFLASAFHEHYVSVPLRMFRILMAFTGMM 436
DB 230 WNIPIHKMVRHAYFFCLIKIKPKVPAIIIFLVSVAHELCIAVPCFLNMAFWGIMF 289
QY 437 QIPLAMFVGRFGQNGNAAVWL-----SLIIGPIAVLMVYVD 475
DB 290 QVPLV-FITNFIQERFGSNVGNMIRBSASCIFGQPMWCGLLYYHD 332
```

```
RESULT 10
US-09-774-639-230
; Sequence 230, Application US/09774639
; Patent No. 6806351
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 230
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-230
```

```
Query Match          21.2%; Score 551; DB 2; Length 163;
Best Local Similarity 89.0%; Pred. No. 5.7e-48;
Matches 105; Conservative 2; Mismatches 5; Indels 6; Gaps 1;
```

```
QY 377 WNIPIVH-----KNCIRHFYKPMRLRGSSKMMARCTGVFLASAFHEHYVSVPLRMFRILMA 430
DB 46 WNAVAVNLIRFPCCPLLCRHFFYKPMRLRGSSKMMARCTGVFLASAFHEHYVSVPLRMFRILMA 105
QY 431 FTGMMAOIPLAMFVGRFGQNGNAAVWLSLIIGPIAVLMVYVDYVLANEAPAAEA 488
DB 106 FTGMMAOIPLAMFVGRFGQNGNAAVWLSLIIGPIAVLMVYVDYVLANEAPAAEA 163
```

```
RESULT 11
US-09-774-639-125
; Sequence 125: Application US/09774639
; Patent No. 6606351
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 125
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (75)
; OTHER INFORMATION: Xaa equals stop translation
US-09-774-639-125
```

```
Query Match          16.6%; Score 431; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.1e-36;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      314 MDYSRIIRLLKLVAVNHLIMLFYWMFHSCINAAVAELMOGDFEFYRDMMNSSTVTF 373
DB      1  MDYSRIIRLLKLVAVNHLIMLFYWMFHSCINAAVAELMOGDFEFYRDMMNSSTVTF 60
OY      374 WNNNIPVHKWCIR 387
DB      61 WNNNIPVHKWCIR 74
```

```
RESULT 12
US-09-165-042-3
; Sequence 3: Application US/09165042
; Patent No. 610077
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L.
; APPLICANT: Oelkers, Peter
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
; TITLE OF INVENTION: ACYLTRANSFERASE
; FILE REFERENCE: 0575/56331
; CURRENT APPLICATION NUMBER: US/09/165,042
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Yeast
US-09-165-042-3
```

```
Query Match          14.5%; Score 375.5; DB 2; Length 522;
Best Local Similarity 26.3%; Pred. No. 2.4e-29;
Matches 127; Conservative 75; Mismatches 189; Indels 91; Gaps 20;
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```
OY      45 DAPAPAP-----NKGDAGVSGHWEILRCHRLDLSFSSDGSFNSYRGILNW-----CVV 94
DB      79 DKPLPPPPPSGLSTRQPSLG-----KQKVFIRKSLDELMVEVQHFRITIMFAGLCVF 134
OY      95 ML-----ILSNARLFE-NLIKYGILVDPQVVS---LFLKDPHSWAPCLVIAANVFA 144
DB      135 IISTLAIDFIDEGRLLEFDLLIFSGQLPLALVTWVPMFLST-----L 178
OY      145 VAAQVEKRLAVGALTEQAGL-LHVNANLATILCFPAVAVLLVESITPVGSLALMAHTI 203
DB      179 LAPQALRLMARGTWATGAGCALLAAHAVVLC-ALPVAHAVERHQLPPASRCVLVFEQV 237
```

```
OY      204 LFL-KLFSY-RDVNSMCRARAKAASAGKASSAAAPHTVSPDNLTYRDLTYFLPAFTL 261
DB      238 RFLMKSYSLFEAAVPGTLRAR-----RREGIQADSFSSY-----LYFLFCPTL 280
OY      262 CYELNFRPSPRIRGRFLRLRLLEMLFFTOLOGLIQOMVPTION-SMKPKMDYSRII 320
DB      281 IYRETYPTPTPVNKNVYAKNFAQALGCVLYACFLGLGCVFVFNMSREPEST--RALV 337
OY      321 ERLKLVAVNHLIMLFYWMFHSCINAAVAELMOGDFEFYRDMMNSSTVTFWNNNIP 380
DB      338 LSIHATILPGIFMLLLIFPALHGMALNFAEMLRFGDBMFRDMMNSTSPSNYRTNNVV 397
OY      381 VHKVCIRHFYKPMLR--RGSSKMMARTGVPLASAFHEHYLVSPLRMR-----LMAFTG 433
DB      398 VHDWLSYVYODGRLIGARAGVAMLGVEFVLSVAHEYIFCFVLGFEFPVMLILFLVIG 457
OY      434 MMAQIPL-----AWVGRPFQGNYNNAVMSLIIGORPVLVYHDYVLYNVEARA 486
DB      458 GMLFMNHDORTGBAW-----NVLMTWMLFLGGIQLVSLYQEWYARRH-CPLP 505
OY      487 EA 488
DB      506 QA 507
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RESULT 13
US-09-949-016-11030
; Sequence 11030: Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11030
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11030
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Query Match          14.5%; Score 375.5; DB 2; Length 522;
Best Local Similarity 26.3%; Pred. No. 2.4e-29;
Matches 127; Conservative 75; Mismatches 189; Indels 91; Gaps 20;
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OY      45 DAPAPAP-----NKGDAGVSGHWEILRCHRLDLSFSSDGSFNSYRGILNW-----CVV 94
DB      79 DKPLPPPPPSGLSTRQPSLG-----KQKVFIRKSLDELMVEVQHFRITIMFAGLCVF 134
OY      95 ML-----ILSNARLFE-NLIKYGILVDPQVVS---LFLKDPHSWAPCLVIAANVFA 144
DB      135 IISTLAIDFIDEGRLLEFDLLIFSGQLPLALVTWVPMFLST-----L 178
OY      145 VAAQVEKRLAVGALTEQAGL-LHVNANLATILCFPAVAVLLVESITPVGSLALMAHTI 203
DB      179 LAPQALRLMARGTWATGAGCALLAAHAVVLC-ALPVAHAVERHQLPPASRCVLVFEQV 237
OY      204 LFL-KLFSY-RDVNSMCRARAKAASAGKASSAAAPHTVSPDNLTYRDLTYFLPAFTL 261
DB      238 RFLMKSYSLFEAAVPGTLRAR-----RREGIQADSFSSY-----LYFLFCPTL 280
OY      262 CYELNFRPSPRIRGRFLRLRLLEMLFFTOLOGLIQOMVPTION-SMKPKMDYSRII 320
DB      281 IYRETYPTPTPVNKNVYAKNFAQALGCVLYACFLGLGCVFVFNMSREPEST--RALV 337
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321 ERLKLAVERNHLIMLIFPYWLFHSCINAAVAELMOFGDREFFYDMNNSSVTYFMQNNIP 380
338 LSLHATIPGIFMLLIPAFILHCLNNAFAEMLRGDRMFYDMNNSISFSNYRTMNV 397
361 VHKWICIRHFYKMLR--RGSSKMMARATGVFLASAFHEHYLVSPLRMFR-----LMAFTG 433
398 VHDMLYSYVQDGLHLLGARARGVAMLGVFVLSAVAHEXIIFCFVLGFFYPVWLLIFLVIG 457
434 MMHQLPL-----AMFGRFQGNVGNAAVWLSLIIGPIAVLMTYHDYVLYNTEAPAA 486
458 GMLNFMWMDORTGPAW-----NYLMTMLFLGGIGVLSYDCQWYARRH-CPUP 505
487 EA 488
506 QA 507

RESULT 14
US-09-326-203A-23
Sequence 23, Application US/09326203A
Patent No. 6444876
GENERAL INFORMATION:
APPLICANT: Lesener, Mike
APPLICANT: Ruzinskiy, Diane
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
FILE REFERENCE: 17045/00/WO
CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 23
LENGTH: 409
TYPE: PRT
ORGANISM: murine
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 270
PAGES: 26192-26201
DATE: 1995
US-09-326-203A-23

Query Match 14.3%; Score 370.5; DB 2; Length 409;
Best Local Similarity 27.5%; Pred. No. 5, 5e-29;
Matches 123; Conservative 69; Mismatches 164; Indels 91; Gaps 18;

71 LQDSIFSSDGSFNSRGLNMCVWML-----SNARLFLR-NLIRYGLVDP 118
4 LIDELFEVD---HIRTIVHMFALLILFVLSITVVDYIDBGRVLEFLLAVARCKPPT 59
119 QV-----VSLFKDPSHPAPCLVIAANVPAARQVEKRLAVGALTQAGLL 166
60 VITWMMAMPFLSTLSIPYFLPDP--W-----AHGYSKSHPLLYSLV-----HGLL 102
167 LHVNLATILCPPAVVLIVSITPVGSLAMARTIIFLKFSYRDVNSWCRARAKAA 226
103 FLVFLQGL-VLGVFPVYVVLATVLPASRFILLBQIRLIMK-----ASHFRENIPRYL 155
227 SAGKASAAAPHTVSYDNLTYRDLYFLFAPFLCYELNFPSPRIKRFILIRILEN- 285
156 NAAEKSSKDPFLPVN-----QYLYFLFAPFLIYRDNYRPTLVWGVAAQFLQVF 207
286 --LFTQVGLIQQMMVPTION-SMKPKMDYSDRIIRLKLAV-----PNHLIMLIF 337
208 GCLFLVYV---IFERLCAPLFRNIRKQBPSS-----ARVAVLCVENSILPGVILFLS 256
338 FYWLFHSCINAAVAELMOFGDREFFYDMNNSSVTYFMQNNIPVHKWICIRHFYKMLR 397

257 FFAFLHCLNNAFAEMLRGDRMFYDMNNSISYSNYRTMNVVHDMLYVYVYKDLMLMF 316
398 SSKW--MARTGVFLASAFHEHYLVSPLR-----MFRIMAFGMAAQIPLMFVGRFPG 450
317 SKRFSAAMLAVALFASAVHEVALAICLSYPYVFLVLFMFPGM---AFNEIVDSRRK 372
451 NYGNAVWLSLIIGPIAVLMTYHDY 477
373 PWNIMVWASLFLGIGLILCFYSQENY 399

RESULT 15
US-09-328-857A-4
Sequence 4, Application US/09328857A
Patent No. 6579974
GENERAL INFORMATION:
APPLICANT: Cases, Sylvaine
APPLICANT: Farese, Robert
APPLICANT: No. 6579974ak, Sabine
APPLICANT: Erickson, Sandra
TITLE OF INVENTION: No. 6579974el Acyl CoA:Cholesterol Acyl
FILE REFERENCE: 6510-104US1
CURRENT APPLICATION NUMBER: US/09/328,857A
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/090,354
PRIOR FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 502
TYPE: PRT
ORGANISM: human
FEATURE:
NAME/KEY: UNSURE
LOCATION: (191)...(191)
OTHER INFORMATION: Xaa is any amino acid
US-09-328-857A-4

Query Match 14.2%; Score 367.5; DB 2; Length 502;
Best Local Similarity 26.7%; Pred. No. 1, 5e-28;
Matches 127; Conservative 64; Mismatches 187; Indels 97; Gaps 20;

45 DAPAPAKDDAGVGSCHWELRCRLQDSIFSSDGSFNSRGLNMCVWML-----IL 98
79 DKPLPDP--PPGSLSELMEXQHRTTYHMF-----IAGLCVFIITSLAIDPI 124
99 SNARLFLR--NLIRYGLVDP 152
125 DEGRLLLEFDPFLIPSPQL--PLALVTWVPMLFST-----LLAPYQALR 166
153 RLAVGALTQAGL--LHVNLATILCPPAVVLIVSITPVGSLAMARTIIFL-KLF 209
167 LMARGTWTOAGTGCALAAHAAVXCAIPHYA--VEHQLPASRCVIVFQVREFLMKSY 224
210 SY-EDVNSWCRARAKASAKKASAAAPHTVSYDNLTYRDLYFLFAPFLCYELNFP 268
225 SFLRAVDPGTRAR-----RGGIOAPSPSS-----LYFLCPFLIYRETYP 267
269 RSPRIKRFILIRILEMLFTQVGLIQQMMVPTION-SMKPKMDYSDRIIRLKLIA 327
268 RTPYRMMVYVAKNFRQALGCVLYACFLIGRLCVFPAFAMSDPFT---RALVSLHAT 324
325 LPGLIFMLLIFFAFLHCLNNAFAEMLRGDRMFYDMNNSISFSNYRTMNVVHDMLYS 384
328 VPHNLIMLIFPYWLFHSCINAAVAELMOFGDREFFYDMNNSSVTYFMQNNIPVHKWICIR 387
365 HFYKMLR--RGSSKMMARATGVFLASAFHEHYLVSPLRMFR-----LMAFTGMAAQIPL 440
385 YVQDGLHLLGARARGVAMLGVFVLSAVAHEXIIFCFVLGFFYPVWLLIFLVIGGMLNPM 444
441 -----AMFGRFQGNVGNAAVWLSLIIGPIAVLMTYHDYVLYNTEAPAAEA 488

Db 445 HDQRTGPAW-----NVLMTWMLFLGGGIQVGLYCOEWYARRH-CPLPQA 487

Search completed: May 5, 2006, 12:35:10
Job time : 49 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 5, 2006, 12:44:55 ; Search time 28 Seconds
(without alignments)
806.677 Million cell updates/sec

Title: US-10-659-800-6
Perfect score: 2594
Sequence: 1 MGDGRSSRRRTGSRPSHG.....VMTYVDYVINYEAAPAAEA 488

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:

1: /SID5/ptodata/1/pubppa/US08_NEW_PUB.pep1.*
2: /SID5/ptodata/1/pubppa/US06_NEW_PUB.pep.*
3: /SID5/ptodata/1/pubppa/US07_NEW_PUB.pep.*
4: /SID5/ptodata/1/pubppa/US08_NEW_PUB.pep.*
5: /SID5/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
6: /SID5/ptodata/1/pubppa/US09_NEW_PUB.pep.*
7: /SID5/ptodata/1/pubppa/US09_NEW_PUB.pep1.*
8: /SID5/ptodata/1/pubppa/US10_NEW_PUB.pep1.*
9: /SID5/ptodata/1/pubppa/US10_NEW_PUB.pep1.*
10: /SID5/ptodata/1/pubppa/US11_NEW_PUB.pep1.*
11: /SID5/ptodata/1/pubppa/US11_NEW_PUB.pep1.*
12: /SID5/ptodata/1/pubppa/US60_NEW_PUB.pep1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2594	100.0	488	US-11-317-983-5	Sequence 5, Appl1
2	2278.5	87.8	498	US-11-317-983-4	Sequence 4, Appl1
3	791.5	30.5	520	US-11-317-983-2	Sequence 2, Appl1
4	779.5	30.1	503	US-11-317-983-9	Sequence 9, Appl1
5	778	30.0	547	US-11-317-983-25	Sequence 25, Appl1
6	656.5	25.3	341	US-11-317-983-8	Sequence 8, Appl1
7	551	21.2	163	US-10-986-501-298	Sequence 98, App
8	431	16.6	74	US-10-986-501-155	Sequence 155, App
9	375.5	14.5	522	US-10-995-561-1030	Sequence 1020, Ap
10	337	13.0	60	US-10-986-501-305	Sequence 305, App
11	259	10.0	48	US-10-986-501-306	Sequence 306, App
12	255	9.8	47	US-10-986-501-307	Sequence 307, App
13	134	5.2	26	US-10-986-501-303	Sequence 304, App
14	118	4.5	9	US-10-986-501-304	Sequence 304, App
15	114.5	4.4	484	US-10-467-657-3820	Sequence 3820, Ap
16	103	4.0	868	US-10-821-234-1082	Sequence 1082, Ap
17	101.5	3.9	432	US-10-992-577-2	Sequence 2, Appl1
18	101.5	3.9	432	US-11-223-294-37	Sequence 37, Appl1
19	100.5	3.9	487	US-11-040-595-6	Sequence 6, Appl1
20	100	3.9	314	US-11-096-568A-20418	Sequence 20418, A
21	98	3.8	17	US-10-986-501-302	Sequence 302, App

22	91.5	3.5	423	11	US-11-079-463-8361	Sequence 8361, Ap
23	91.5	3.5	4097	9	US-10-501-035-263	Sequence 263, App
24	91	3.5	449	11	US-11-079-463-5270	Sequence 5270, Ap
25	90.5	3.5	482	11	US-11-072-512-3794	Sequence 3794, Ap
26	90	3.5	673	9	US-10-055-877-321	Sequence 321, App
27	89.5	3.5	615	9	US-10-821-234-873	Sequence 873, App
28	89	3.4	369	9	US-10-506-454-749	Sequence 749, App
29	89	3.4	516	11	US-11-168-298-20291	Sequence 20291, A
30	88.5	3.4	4128	9	US-10-770-726-77	Sequence 77, Appl1
31	88	3.4	381	11	US-11-096-568A-10876	Sequence 10876, A
32	88	3.4	400	9	US-10-454-437-306	Sequence 306, App
33	88	3.4	423	9	US-10-454-437-304	Sequence 304, App
34	88	3.4	461	11	US-11-079-463-9682	Sequence 9682, Ap
35	87	3.4	831	7	US-09-941-095-5	Sequence 5, Appl1
36	87	3.4	831	11	US-11-198-746-5	Sequence 5, Appl1
37	87	3.4	831	11	US-11-198-794-5	Sequence 5, Appl1
38	87	3.4	831	11	US-11-193-211-5	Sequence 5, Appl1
39	87	3.4	831	11	US-11-198-657-5	Sequence 5, Appl1
40	86.5	3.3	486	11	US-11-168-298-13811	Sequence 13811, A
41	86.5	3.3	2589	11	US-11-216-660-9	Sequence 9, Appl1
42	86	3.3	330	11	US-11-110-274-4	Sequence 35, Appl1
43	86	3.3	330	11	US-11-040-218-35	Sequence 35, Appl1
44	86	3.3	344	11	US-11-040-218-37	Sequence 37, Appl1
45	86	3.3	346	11	US-11-040-218-39	Sequence 39, Appl1

ALIGNMENTS

RESULT 1						
US-11-317-983-5						
Sequence 5, Application US/11317983						
Publication No. US20060090222A1						
GENERAL INFORMATION:						
APPLICANT: Zou, Jitao						
APPLICANT: Taylor, David C						
APPLICANT: Wei, Yangdou						
APPLICANT: Jako, Collette C						
TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants						
FILE REFERENCE: 3015-5684,1US						
CURRENT APPLICATION NUMBER: US/11/317,983						
CURRENT FILING DATE: 2005-12-23						
PRIOR APPLICATION NUMBER: US/11/117,005						
PRIOR FILING DATE: 2005-04-28						
PRIOR APPLICATION NUMBER: 09/623,514						
PRIOR FILING DATE: 2001-03-29						
PRIOR APPLICATION NUMBER: PCT/CA99/01202						
PRIOR FILING DATE: 1999-12-16						
PRIOR APPLICATION NUMBER: 60/112,812						
PRIOR FILING DATE: 1998-12-17						
NUMBER OF SEQ ID NOS: 26						
SOFTWARE: PatentIn Ver. 2.1						
SEQ ID NO 5						
LENGTH: 488						
TYPE: PRT						
ORGANISM: human						
US-11-317-983-5						
Query Match						
Best Local Similarity 100.0%; Score 2594; DB 10; Length 488;						
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	MGDGRSSRRRTGSRPSHG	GGGPAAEEDVDAAGDVGAAADGAPAPAPKDDAGVG	60		
DB	1	MGDGRSSRRRTGSRPSHG	GGGPAAEEDVDAAGDVGAAADGAPAPAPKDDAGVG	60		
QY	61	SGHWEIARCRLODSIFSSDSGFSNVRGILN	CVVWLISNARLFLENLTKYGIIVDPLOY	120		
DB	61	SGHWEIARCRLODSIFSSDSGFSNVRGILN	CVVWLISNARLFLENLTKYGIIVDPLOY	120		
QY	121	VSLFLKDPHSPAPCLVTIAANVFVAFAV	QVEKRLAVGALTTEOAGILLHVANLATILCPA	180		
DB	121	VSLFLKDPHSPAPCLVTIAANVFVAFAV	QVEKRLAVGALTTEOAGILLHVANLATILCPA	180		
QY	121	VSLFLKDPHSPAPCLVTIAANVFVAFAV	QVEKRLAVGALTTEOAGILLHVANLATILCPA	180		
DB	121	VSLFLKDPHSPAPCLVTIAANVFVAFAV	QVEKRLAVGALTTEOAGILLHVANLATILCPA	180		

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Qy 181 AVTLVESITPVGSLALMAHTILFLKLFSDYDVNSMCRBARAKASAGKASAAAPHT 240
    |||
Db 181 AVTLVESITPVGSLALMAHTILFLKLFSDYDVNSMCRBARAKASAGKASAAAPHT 240
Qy 241 VSYPDNLTYRDLYFLFAPTLCEYNLPPSPRIKRFLLRILEMLFTQLQVGLIQQM 300
    |||
Db 241 VSYPDNLTYRDLYFLFAPTLCEYNLPPSPRIKRFLLRILEMLFTQLQVGLIQQM 300
Qy 301 VPTIOMSKPDKMDYSRIERLLKLAVERNHLIMLFFYWLPHSCLNVAELMOGDERF 360
    |||
Db 301 VPTIOMSKPDKMDYSRIERLLKLAVERNHLIMLFFYWLPHSCLNVAELMOGDERF 360
Qy 361 YRDWNSSESVTFWQNNMIPVHKCIRHFYKPMLRGSSKMMARTGVFLASAFHEYLVS 420
    |||
Db 361 YRDWNSSESVTFWQNNMIPVHKCIRHFYKPMLRGSSKMMARTGVFLASAFHEYLVS 420
Qy 421 VPLRMFLMAFTGMAAOIPLAMFVGRFQGNYGNAVWLSLIIGQPIAVLAMYHDYVVLN 480
    |||
Db 421 VPLRMFLMAFTGMAAOIPLAMFVGRFQGNYGNAVWLSLIIGQPIAVLAMYHDYVVLN 480
Qy 481 YEAPAAEA 488
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Db 481 YEAPAAEA 488

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RESULT 2

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US-11-317-983-4
; Sequence 4, Application US/11317983
; Publication No. US20060090222A1
; GENERAL INFORMATION:
; APPLICANT: Zou, Jitao
; APPLICANT: Taylor, David C
; APPLICANT: Wei, Yangdou
; APPLICANT: Jako, Colette C
; TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
; FILE REFERENCE: 3015-5684, IUS
; CURRENT FILING DATE: 2005-12-23
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/11/117,005
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 09/623,514
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/CA99/01202
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/112,812
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 498
; TYPE: PRT
; ORGANISM: mouse
US-11-317-983-4

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Query Match 87.8%; Score 2278.5; DB 10; Length 498;
 Best Local Similarity 85.1%; Pred. No. 8.8e-196;
 Matches 421; Conservative 29; Mismatches 34; Indels 11; Gaps 3;

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Qy 1 MGDR---GSSRRRTGSSPSHGGCGPAAAEEDVDAAGPDVGAAGAPAPAP----- 51
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Db 1 MGDRGAGSSRRRTGSSPSHGGCGPAAAEEDVDAAGPDVGAAGAPAPAPAPAPAPAPAPATR 60
Qy 52 NKDDGAGVSGSHWELRCRLDLSFSSDSGFENYGIIMCVMLILSNARLFLENLKY 111
    |||
Db 61 DKDGTSTVGDWDLRCHRLDLSFSSDSGFENYGIIMCVMLILSNARLFLENLKY 120
Qy 112 GILVDPIDVSLFLKDPHSPAPCLVIANVPAVAFOVEKRLAVGALTEQAGLLAHVAN 171
    |||
Db 121 GILVDPIDVSLFLKDPHSPAPCLVIANVPAVAFOVEKRLAVGALTEQAGLLAHVAN 180
Qy 172 LATICPPAAVVLVESITPVGSLALMAHTILFLKLFSDYDVNSMCRBARAKASAG 229
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Db 181 LATICPPAAVVLVESITPVGSLALMAHTILFLKLFSDYDVNSMCRBARAKASAG 240
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    |||
Db 241 KVSAGAAAOAVSYPDNLTYRDLYFLFAPTLCEYNLPPSPRIKRFLLRILEMLFT 300
Qy 290 QLOVGLIQQMWVPTIOMSKPDKMDYSRIERLLKLAVERNHLIMLFFYWLPHSCLNAV 349
    |||
Db 301 QLOVGLIQQMWVPTIOMSKPDKMDYSRIERLLKLAVERNHLIMLFFYWLPHSCLNAV 360
Qy 360 AELMOGDERFERYRDWNSSESVTFWQNNMIPVHKCIRHFYKPMLRGSSKMMARTGVFL 409
    |||
Db 361 AELMOGDERFERYRDWNSSESVTFWQNNMIPVHKCIRHFYKPMLRGSSKMMARTGVFL 420
Qy 420 ASAFHEYLVSVPRLMFLMAFTGMAAOIPLAMFVGRFQGNYGNAVWLSLIIGQPIAV 469
    |||
Db 421 TSAPFHEYLVSVPRLMFLMAFTGMAAOIPLAMFVGRFQGNYGNAVWLSLIIGQPIAV 480
Qy 470 LMYVDYVVLN YEAP 484
    |||
Db 481 LMYVDYVVLN YEAP 495

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RESULT 3

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US-11-317-983-2
; Sequence 2, Application US/11317983
; Publication No. US20060090222A1
; GENERAL INFORMATION:
; APPLICANT: Zou, Jitao
; APPLICANT: Taylor, David C
; APPLICANT: Wei, Yangdou
; APPLICANT: Jako, Colette C
; TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
; FILE REFERENCE: 3015-5684, IUS
; CURRENT FILING DATE: 2005-12-23
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/11/117,005
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 09/623,514
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/CA99/01202
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/112,812
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-317-983-2

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Query Match 30.5%; Score 791.5; DB 10; Length 520;
 Best Local Similarity 38.0%; Pred. No. 8.7e-63;
 Matches 194; Conservative 77; Mismatches 174; Indels 65; Gaps 17;

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Qy 8 RRRRTGSSPSHGG-----GGPAAAEEDVDAAGPDVGAAGAPAPAP----- 48
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Db 25 RLRKRKSSDSNGLLSGSDNNSPSDDVGAAPADVRRLDSDVDDAG--TANLAGDNG 83
Qy 49 PAPNKDAGVSGSHWELRC-----HRLDLSFSSDSGF--SNYRGIIMCVML 96
    |||
Db 84 GDDNNGGGRGGEGGNGADATFTYRPSVPAHRRARRESPLSDAIFKOSHAGLFNLCVVVL 143
Qy 97 ILSNARLFLENLKYGILV-DPIQVSLFLKDPHSPAPCLVIANVPAVAFOVEKRLA 155
    |||
Db 144 IAVNSRLILENLMRYGWLIRTFDFWSSSLRD---WPLFMCCISLSTFPLAAFTVEKVL 200
Qy 156 VGALTEQAGLLAHVANLATICPPAAVVLVESITPVGSLALMAHTILFLKLFSDYR-- 212
    |||
Db 201 OKYISEPVVFLHIIITMTVELVPEYVYTLRCDSAFSLGSVTLMULT--CIWMLKTVSYAITS 259
Qy 213 -DVNSMCRBARAKASAGKASAAAPHTVSYPDNLTYRDLYFLFAPTLCEYNLPPSP 271

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Db      260 YDIRS-----LANAADKANP-----EVSY--YVSLKSLAVFMVAFTLCYOPSPRSBA 304
Qy      272 RIRKFLRLRIEMFFPOLQVGLIQOMNVPTIOMSKPKF-DMDYSRIERBLKLAVERN 330
Db      305 CIRKMWVARQPKLVIFGFMGFIIEQYINPVRNSKHLKGDLLYA--IEEVLKLSVNN 362
Qy      331 HLIWLIFFYWLPHSCINAVAEIMQFDRREFYRDMMNSESUTYFWQWNI PVHKMCIRHPY 390
Db      363 LYVWLCMYCFPHMLNLIABELLCFODREFYKDMNNAKSGDYWRKMNPPVKMVRHY 422
Qy      391 KEMLRGSSKMMARTGVFLASAPFHEYLVSPLRMFRMAFTGMAQIPLAMFVGRFPG 450
Db      423 FPCLRSKLPKTLAIIIAFLVASVFBELCIAVPCRLFKLWAFGIMFQVPLV-FITVYLOE 481
Qy      451 NY-----GNAAVW-LSLIIGQPIAVLMYVHD 475
Db      482 RFGSTVGNNIFWIFCIFIQGPWCVLYYHD 511
```

RESULT 4

```
US-11-317-983-9
; Sequence 9, Application US/11317983
; Publication No. US2006090222A1
; GENERAL INFORMATION:
; APPLICANT: Zou, Jitao
; APPLICANT: Taylor, David C
; APPLICANT: Wei, Yangdou
; APPLICANT: Juko, Colette C
; TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
; FILE REFERENCE: 3015-5684.1US
; CURRENT APPLICATION NUMBER: US/11/317,983
; PRIOR FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: US/11/117,005
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 09/623,514
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/CA99/01202
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/112,812
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Brassica napus
US-11-317-983-9
```

Query Match 30.1%; Score 779.5; DB 10; Length 503;

Best Local Similarity 38.7%; Pred. No. 9.8e-62;

Matches 191; Conservative 83; Mismatches 168; Indels 51; Gaps 15;

```
Qy      10 RRTGSRPSSHG-----GGPAAAEBEVDAAGPDV-GAAGDAPAPAKDGDGV 59
Db      26 RKRSSSDSNGLSTPSDSDVGAABERDRDAABEAGTANLAGDADTRRSAGS- 84
Qy      60 GSGHWEELRC-----HRLQDSLFFSSDSGF-SYRGLMKCVMLLSNARLLENLI 109
Db      85 ----DVAFYRPSVPAHRRRTRESPLSDAIFKQSHAGLFNLCVVVLVAVNSRLIENIM 139
Qy      110 KYGILV-DPIQVSLFLKDPHSMWPACLVIANVAVAVAFOVERKRLVAGALTEQAGLLH 168
Db      140 KYGMLIRIDPWFSSISLRD--WPLFMCCLSLVFPLAFTVEKRVLOKFTISEPVAIIH 196
Qy      169 VAKIATILCFPAAVLVLESITPVGSLALMAHTILFLKPSYRDVNSGCRARAKAASA 228
Db      197 VITWTEVLYPYVTLRCDSAVLGSVTMLLTL-CIVMLKLVSAHTS--YDIRLTAASA 252
Qy      229 GKXASSAAAPRTVSPDULYRDLYYFLFAPTLCELANPPSPRIKGFLLRIILEMFF 288
Db      253 DK-----VDPEISY--YVSLKSLAVFMVAFTLCYOPSPRSACIRKMWVARQPKLVIF 304
```

```
Qy      289 TOLQVGLIQOMNVPTIOMSKPKF-DMDYSRIERBLKLAVERNHLIWLIFPYWLPHSCIN 347
Db      305 TGLMGPFIIEQYINPVRNSKHLKGDLLYA--IEEVLKLSVNNLVYWLCMFCFPHMLN 362
Qy      348 AVAEIMQFDRREFYKDMNNSVITYFWQWNI PVHKMCIRHPYKEMLRGSSKMMARTGV 407
Db      363 IIAELLCGDRREFYKDMNNAKSGDYWRKMNPPVKMVRHYFPCLRIRIKRVPAILYA 422
Qy      408 FLASAPFHEYLVSPLRMFRMAFTGMAQIPLAMFVGRFPGQNGNAVWL-----SLI 462
Db      423 FLVASVFBELCIAVPCRLFKLWAFGIMFQVPLV-FITVLOERFGSGVGNMIFGSASCI 481
Qy      463 ICGQPIAVLMYVHD 475
Db      482 RCGPWCGLYYHD 494
```

RESULT 5

```
US-11-317-983-25
; Sequence 25, Application US/11317983
; Publication No. US2006090222A1
; GENERAL INFORMATION:
; APPLICANT: Zou, Jitao
; APPLICANT: Taylor, David C
; APPLICANT: Wei, Yangdou
; APPLICANT: Juko, Colette C
; TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
; FILE REFERENCE: 3015-5684.1US
; CURRENT APPLICATION NUMBER: US/11/317,983
; PRIOR FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: US/11/117,005
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 09/623,514
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/CA99/01202
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: 60/112,812
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-317-983-25
```

Query Match 30.0%; Score 778; DB 10; Length 547;

Best Local Similarity 36.1%; Pred. No. 1.5e-61;

Matches 194; Conservative 77; Mismatches 174; Indels 92; Gaps 17;

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Qy      8 RRRRTGSRPSSHG-----GGPAAAEBE-----VRDAAAGPDVGAAGDAPA 48
Db      25 RLRRKSRSDSNGLLSGSDNNSPSDVGAPADVRDIDSVVNDAGG-TANLAGDNNG 83
Qy      49 PAPNKGAGVAGSGHWEELRC-----HRLQDSLFFSSDSGF----- 82
Db      84 GGDNNGGRGGBEGNADATFYRPSVPAHRRARESPLSDAIFKQSHAGLFNLCVVVL 143
Qy      83 ----SNRYGILMKCVMLLSNARLLENLIKYGILV-DPIQVSLFLKDP 128
Db      144 IAVNSRLIENIMKSHAGLFNLCVVVLIAVNSRLIENIMKGMWIRIDPWFSSISLRD- 202
Qy      129 HSWPAPCLVIANVAVAVAFOVERKRLVAGALTEQAGLLHYVANLATILCFPAAVLVLES 188
Db      203 --WPLFMCCLSLVFPLAFTVEKRVLOKFTISEPVAIIITWTEVLYPYVTLRCDS 260
Qy      189 ITPVGSILALMAHTILFLKPSYR-----DVNSWCRARAKAASGKXASSAAAPRTVSGP 244
Db      261 AFLGSVTMLLTL-CIVMLKLVSAHTSYDIRS-----LANAADKANP-----EVSY- 305
Qy      245 DNLTYRDLYYFLFAPTLCELANPPSPRIKGFLLRIILEMFFPOLQVGLIQOMNVPTI 304
Db      306 --YVSLKSLAVFMVAFTLCYOPSPRSACIRKMWVARQPKLVIFGFMGFIIEQYINPDI 364
```

```
OY 305 QNWKPKF-DMDYSRIERLLKLAVERNHLIMLFFPYWLFHSCLNAVELMORGDEPRD 363
DB 365 RNSKPELGDLLYA--IERVLKLSVPLNYVLCMFYCFEHLMLNLAEILCGDREFFKD 422
OY 364 WNNSESVTYFQWNNNIPVHKCIRHFYKPMRLRGSSKMMARTGVFLASAFHEYLVSPL 423
DB 423 WNNKSVGDYVRMMNMPHKMMVRIITFPCLRSKIPKTLAIITAVLSAVFHELCIAVPC 482
OY 424 RMFRMATGMAOIPLAMPVGRFFQGNV---GNAAVW-LSLIGOPIAVLMYVHD 475
DB 483 RLFPKMAELGIMFOVPLV-FITNVLQERFGSVGMIMFIFCIGFQPCVCLLYHD 538
```

RESULT 6
US-11-317-983-8

```
; Sequence 8, Application US/11317983
; Publication No. US20060090222A1
; GENERAL INFORMATION:
; APPLICANT: Zou, Jitao
; APPLICANT: Taylor, David C
; APPLICANT: Wei, Yangdou
; APPLICANT: Jako, Colette C
; TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
; FILE REFERENCE: 3015-5684.1US
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: US/11/317,983
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 09/623,514
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/CA99/01202
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/112,812
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Brassica napus
; US-11-317-983-8
```

Query Match 25.3%; Score 656.5; DB 10; Length 341;
Best Local Similarity 41.9%; Pred. No. 66-51;
Matches 144; Conservative 62; Mismatches 117; Indels 21; Gaps 8;

```
OY 138 IAAVFAVAFAQVEKRLAVGALTQAGLLHVAANLATTLCFPAAVLLVESTTPVGSLLA 197
DB 4 LLSIFPLAAFTVELVLOKICSEPVIFLHVITMTFVLVYVYVTLCDSAFLSGDTLM 63
OY 198 LMAHTILFLKLPSTYDVNWKCRARAKASACKRSSAAAPHTVSPDNLTRDYLYPLF 257
DB 64 LLT-CIVLKLVSAVHTNYDIR---TLANSSDKNP-----EVSY--YVSLKSLAYFML 111
OY 258 APTLCYELNFPSPRIKRFILRLILEMLFTQLQVGLIQWNVVTIONSMKPKF-DMDY 316
DB 112 APTLCYOSYRSRPSIRKGMVARQAKVITFGLMGFITIEQYINIVANSKRPKGLDLY 171
OY 317 SRIERLLKLAVERNHLIMLFFPYWLFHSCLNAVELMORGDEPRDWMNSESVTYFQW 376
DB 172 A--IERVLKLSVPLNYVLCMFYCFEHLMLNLAEILCGDREFFKDWNNKSVGDYVRM 229
OY 377 WNIPIHKCIRHFYKPMRLRGSSKMMARTGVFLASAFHEYLVSPLMFRMAFTGMA 436
DB 230 WNNPDKMMVRRHVFPCLRIKIPKVPALITAVLSAVFHELCIAVPCDLPNLMAGTME 289
OY 437 QIPLAMPVGRFFQGNVGNAAVWL-----LSLIGOPIAVLMYVHD 475
DB 290 QVPLV-FITNVLQERFGSVGMIMGASGSCIFGQPCVCLLYHD 332
```

RESULT 7

US-10-986-501-298
; Sequence 298, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:

```
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 298
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-986-501-298
```

Query Match 21.2%; Score 551; DB 9; Length 163;
Best Local Similarity 89.0%; Pred. No. 6,56-42;
Matches 105; Conservative 2; Mismatches 5; Indels 6; Gaps 1;

```
OY 377 WNIPIH-----KWCIRHFYKPMRLRGSSKMMARTGVFLASAFHEYLVSPLMFRMA 430
DB 46 WNNVNLNRFPCPLCRHFYKPMRLRGSSKMMARTGVFLASAFHEYLVSPLMFRMA 105
OY 431 FTGMAOIPLAMPVGRFFQGNVGNAAVWL$LLIGOPIAVLMYVHDYVLTAEAPAEA 488
DB 106 FTGMAOIPLAMPVGRFFQGNVGNAAVWL$LLIGOPIAVLMYVHDYVLTAEAPAEA 163
```

RESULT 8
US-10-986-501-155
; Sequence 155, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:

```
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
```

PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 373
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 155
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
US-10-986-501-155

Query Match 16.6%; Score 431; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e-31;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 314 MDYRIIERLLKLVNPHLILFIYWLPHSCNAAVAELMQFGDREFYRDMMNSSEVTYF 373
Db 1 MDYSRIIERLLKLVNPHLILFIYWLPHSCNAAVAELMQFGDREFYRDMMNSSEVTYF 60
Qy 374 WQNNIPVHKWCIR 387
Db 61 WQNNIPVHKWCIR 74

RESULT 9
US-10-995-561-1030
Sequence 1030, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ. ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1030
LENGTH: 522
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-1030

Query Match 14.5%; Score 375.5; DB 9; Length 522;
Best Local Similarity 26.3%; Pred. No. 1.4e-25;
Matches 127; Conservative 75; Mismatches 189; Indels 91; Gaps 20;

Qy 45 DAPAPAP-----NKGDAGVSGHMEIRLQDLSFSDGFGNRYGILNM-----CVV 94
Db 79 DKUPPPPPPSLSSTQPSLSG----KQVFIKRSLLDELMVEVGFRTIYMFIAGLCVF 134
Qy 95 ML-----IISNAFLIE-NIKYGIIVDPIQVS---LFLKDPHSPAPCLVIANVFA 144
Db 135 IISTLAIDFIDEGRLLEFDLILFSGQLPLATVTWPMFLST-----L 178
Qy 145 VAAFOVEKRLAVGLTEQAGI-LHVNANLITLCFPAVVLVSITPVGSLAMMTI 203
Db 179 LAPQALRLMARGTGTATGAGCALLAAHAVALC-ALPVHAVERHQPPASRCVLVEQV 237
Qy 204 LFL-KLFSY-RDVSMCRARAKAASAGKASAAAPHTVSYPNLTLYRDLVYFLFAPTL 261
Db 238 RFLMKSYSPLEAENPGTLRAR-----RGEQGAQSFSSY-----LYLFCPTL 280
Qy 262 CYELNPRSPRIKRFILRLILELFTQLOVGLIQGMVPTTON-SMKPKMDYSRII 320
Db 281 IYRETYVRTPEYRWNVYAKNFAQALGCVLACFTIGRLCVVPANMSREPFST---DALV 337

Qy 321 ERLIKLVNPHLILFIYWLPHSCNAAVAELMQFGDREFYRDMMNSSEVTYFQNNIP 380
Db 338 LSLIHATLPGIFMLLILFPALFHQWLAFAEMLFGDRMFFRDMNNSGFSNRYRTNNV 397
Qy 381 VHKWCIRHFKYKPMIR--RGSSKMARFGVFLASAFHEHYLVSPDNRFR----LMAFTG 433
Db 398 VHDWLYSVYQDGRILRGARARGVAMGVFLVSAVAHEHYICFVYLGFFYPVMLILFLVIG 457
Qy 434 MMAQIPL-----AMFVGRFGQNYGNAAVWLSLIIGQPIAVLVMYHYDVVLYNEAPAA 486
Db 458 GMLNFMHMDORTGPAM-----NVLMTWMLFLGQGIQVSLYCOEWYARRH-CLLP 505
Qy 487 EA 488
Db 506 QA 507

RESULT 10
US-10-986-501-305
Sequence 305, Application US/10986501
Publication No. US20050244845A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P2C1
CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 373
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 305
LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
US-10-986-501-305

Query Match 13.0%; Score 337; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.5e-23;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 310 PKMDYSRIIERLLKLVNPHLILFIYWLPHSCNAAVAELMQFGDREFYRDMMNSSE 369
Db 1 PKMDYSRIIERLLKLVNPHLILFIYWLPHSCNAAVAELMQFGDREFYRDMMNSSE 60

RESULT 11
US-10-986-501-306
Sequence 306, Application US/10986501
Publication No. US20050244845A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins

```
FILE REFERENCE: P2013P2C1
CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 306
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
US-10-986-501-306

Query Match
Best Local Similarity 10.0%; Score 259; DB 9; Length 48;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      387 RHFFKPMRLRSGSCWMARGTGVLASAPFHEHYLVSPILMFELMAFTGN 434
Db      1 RHFFKPMRLRSGSCWMARGTGVLASAPFHEHYLVSPILMFELMAFTGN 48

RESULT 12
US-10-986-501-307
Sequence 307, Application US/10986501
Publication No. US20050244845A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P2C1
CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 373
```

```
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 307
LENGTH: 47
TYPE: PRT
ORGANISM: Homo sapiens
US-10-986-501-307

Query Match
Best Local Similarity 9.8%; Score 255; DB 9; Length 47;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      435 MAQPLAMFVGRFGQNGYNAAVWLSLITGQPIAVLMTYHDYVLYN 481
Db      1 MAQPLAMFVGRFGQNGYNAAVWLSLITGQPIAVLMTYHDYVLYN 47

RESULT 13
US-10-986-501-303
Sequence 303, Application US/10986501
Publication No. US20050244845A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P2C1
CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 373
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 303
LENGTH: 26
TYPE: PRT
ORGANISM: Homo sapiens
US-10-986-501-303

Query Match
Best Local Similarity 5.2%; Score 134; DB 9; Length 26;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      284 EMLEFTOLQVGLIQOMVVPITQNSMK 309
Db      1 EMLEFTOLQVGLIQOMVVPITQNSMK 26

RESULT 14
US-10-986-501-304
Sequence 304, Application US/10986501
Publication No. US20050244845A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P2C1
CURRENT APPLICATION NUMBER: US/10/986,501
```

```
/ CURRENT FILING DATE: 2004-11-12
/ PRIOR APPLICATION NUMBER: US/10/621,363
/ PRIOR FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/969,730
/ PRIOR FILING DATE: 2001-10-06
/ PRIOR APPLICATION NUMBER: 09/774,639
/ PRIOR FILING DATE: 2001-02-01
/ PRIOR APPLICATION NUMBER: 60/238,291
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 09/244,112
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: PCT/US98/16235
/ PRIOR FILING DATE: 1998-08-04
/ PRIOR APPLICATION NUMBER: 60/056,371
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,732
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,366
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 373
/ SOFTWARE: Patencin Ver. 2.0
/ SEQ ID NO 304
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-986-501-304
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Query Match          4.5%; Score 118; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      370 VTTFWQNNNIPVHKWCIR 387
Db      1 VTTFWQNNNIPVHKWCIR 18
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RESULT 15
US-10-467-657-3820
/ Sequence 3820, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASNIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqMin99, version 1.04
/ SEQ ID NO 3820
/ LENGTH: 484
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3820
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Query Match          4.4%; Score 114.5; DB 9; Length 484;
Best Local Similarity 19.2%; Pred. No. 0.027;
Matches 92; Conservative 56; Mismatches 152; Indels 179; Gaps 22;
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QY      131 WPAFLVIAANFAV-----AAFOYKRLAVGALTEAGLLHYANLATIICPPAA 181
Db      5 WFMPLISVFAFLFVLPDITWGFAPKPSVQNLIL--LAAGGWLHYHISPV-----FAHI 57
QY      182 VLVLVESITPVGSLIAL-----MAHTILFLKLFESYRDVNSWCRARAKAASA 228
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Db      58 IVLVSSCVYLIGELILRSDESTRRFRLGCGIASSITVLGFYKYPD---FFRDLIAQYAGK 114
QY      229 GKXASSAABHTVSYPDNLTYRDLVYFLF---AP-----TLCYELNF----- 267
Db      115 G-GAIDIMPLGLSY---YTFOSVAVLYVCPPAPHAARFGMBELHLHLSFFPTVTSGPII 170
QY      268 -----PSPRIKRKFLRLILEMLFTQIQVGLI-QQMMVPT 303
Db      171 RAAAFKSTDEQAGALAQIRTRPRSP--VRPALAVSLILGLIAKKKWLGLIAENNVSPV 229
QY      304 ION-----SKKPFQMD-YSRIT--ERLLKLAVPNHLIWLIFFYWLFH 343
Db      230 FENPTQFDGSGVLAGVYGYTFQLFLDFSGSDLVIGMMLLGFRLPKN-----FS 279
QY      344 SCLNVAELMQRGDEFRDMWNSSVYTFQNNNIPVHKWCIRRFYKPMRLRGSSKXMA 403
Db      280 APLRAA-----NIRAFWKHISLSTWTRDYIYIPL--GSSKKGEL 318
QY      404 RT-----GVFLASAPFHEY-----LVSVPLRMFRLMAFTGMAQIPLAM 442
Db      319 RTQNLMAAMVLSGIMHGYGNFLIWGALHGTALALNTGDRYFGRDALCRKLYLAPLSW 378
QY      443 EV-----GRFFQGNYGNAAYV-----LSLIIGQPIAVLMTYVDY 476
Db      379 FVTFHFVCLSFYVNTANPDADGAVFSALFANAGGMNAFORADMILLASFASIMLLYPY 437
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Job time : 29 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: May 7, 2006, 02:54:45 ; Search time 1155 Seconds
(without alignments)
5240.853 Million cell updates/sec

Title: US-10-659-800-6
Perfect score: 2534
Sequence: 1 MGDGSSRRRTGSRPSHG.....VLMVHYDYVLYNPAEAAEA 488

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 14089978

Minimum DB seq length: 0
Maximum DB seq length: 500

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcp -NORM=ext
-HEADSIZE=500 -MINLEN=0 -MAXLEN=500 -HOST=abss07
-USER=US10659800@cgn1_1.1026@runat_05052006_122318_17444 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	842	32.5	452	3	US-09-867-701-4664 Sequence 4664, Ap
2	612	23.6	371	3	US-09-867-701-5894 Sequence 5894, Ap
3	603.5	23.3	433	3	US-09-764-853-314 Sequence 314, App
4	567	21.9	447	3	US-09-918-995-29256 Sequence 29256, A
5	374	14.4	201	8	US-10-741-600-12886 Sequence 12886, A
6	374	14.4	201	8	US-10-741-600-12898 Sequence 12898, A
7	332	12.8	471	3	US-09-918-995-1979 Sequence 1979, Ap

8	330.5	12.7	380	3	US-09-770-791-192 Sequence 192, App
9	321	12.4	201	8	US-10-741-600-12888 Sequence 12888, A
10	321	12.4	201	8	US-10-741-600-12894 Sequence 12894, A
11	321	12.4	201	8	US-10-741-600-12900 Sequence 12900, A
12	321	12.4	201	8	US-10-741-600-12905 Sequence 12905, A
13	290.5	11.2	362	7	US-10-424-599-115051 Sequence 115051, A
14	288	11.1	201	8	US-10-741-600-12887 Sequence 12887, A
15	288	11.1	201	8	US-10-741-600-12893 Sequence 12893, A
16	288	11.1	201	8	US-10-741-600-12899 Sequence 12899, A
17	288	11.1	201	8	US-10-741-600-12904 Sequence 12904, A
18	274	10.6	201	8	US-10-741-600-46499 Sequence 46499, A
19	274	10.6	201	8	US-10-741-600-46522 Sequence 46522, A
20	245	9.4	201	8	US-10-741-600-46592 Sequence 46592, A
21	232	8.9	299	5	US-10-157-855-13 Sequence 13, App1
22	232	8.9	299	5	US-10-647-517-22 Sequence 22, App1
23	217	8.4	121	6	US-10-029-386-25717 Sequence 25717, A
24	197.5	7.6	381	5	US-10-157-885-20 Sequence 20, App1
25	197.5	7.6	381	9	US-10-647-517-12 Sequence 12, App1
26	191.5	7.4	393	3	US-09-918-995-33739 Sequence 33739, A
27	191.5	7.4	399	3	US-09-918-995-33281 Sequence 33281, A
28	191.5	7.4	401	3	US-09-918-995-33158 Sequence 33158, A
29	191.5	7.4	418	3	US-09-918-995-33158 Sequence 33158, A
30	188.5	7.3	401	3	US-09-918-995-33355 Sequence 33355, A
31	187.5	7.2	401	3	US-09-918-995-33843 Sequence 33843, A
32	181	7.0	470	3	US-09-770-444-209 Sequence 209, App
33	177.5	6.8	365	3	US-09-918-995-34424 Sequence 34424, A
34	173.5	6.7	402	3	US-09-918-995-33444 Sequence 33444, A
35	173.5	6.7	445	8	US-10-425-115-119521 Sequence 119521, A
36	171.5	6.6	378	6	US-10-369-493-30172 Sequence 30172, A
37	170	6.6	275	5	US-10-157-885-5 Sequence 5, App1
38	170	6.6	275	9	US-10-647-517-17 Sequence 17, App1
39	164.5	6.3	383	3	US-09-918-995-35056 Sequence 35056, A
40	159	6.1	421	3	US-09-878-134-110 Sequence 110, App1
41	155	6.0	253	5	US-10-157-885-7 Sequence 7, App1
42	155	6.0	253	9	US-10-647-517-27 Sequence 27, App1
43	130.5	5.0	408	3	US-09-918-995-34099 Sequence 34099, A
44	130	5.0	201	8	US-10-741-600-46504 Sequence 46504, A
45	130	5.0	201	8	US-10-741-600-46517 Sequence 46517, A

ALIGNMENTS

RESULT 1
US-09-867-701-4664
; Sequence 4664, Application US/09867701
; Patent No. US2002012237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4664
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4664

Alignment Scores:
Pred. No.: 4.2e-86
Score: 842.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 32.5%
DB: 3
Gaps: 0

US-10-659-800-6 (1-488) x US-09-867-701-4664 (1-452)

Length: 452
Matches: 150
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

QY	253	LYTFTYRPhLeuPheAlaProThiLeuCYuTYGJuLeuAlaPheProAlaSerProArg	272
Db	3	TACTACTCTCTCTCCGCCCCACCTGTGTGTACAGCTCACTTTCGCCCTCCGCCG	62
QY	273	ILeArgLYaRgPheLeuLeuArgJLeLeuGJuMetLeuPhePheThrgJnLeuGln	232
Db	63	ATCCGGAAACGGCTTTTGCTGGCGAGCGGATCTTGAGATGCTGTTCCTCACCCAGCTCAG	122
QY	293	VALGYLeuIIeGInGInTrpMetValProThriIIeGInAlaAsnSerMetLYsProPheLYs	312
Db	123	GTGGGGCTATCATCAGACGTGAAGTGTCCCACTCATCAAACTCCAAGAAAGCCCTTCAG	182
QY	313	AspMetAspTrsSerArgJLeIeGJuArgLeuLeuLYaLeuAlaValProAlaHisLeu	332
Db	183	GACATGGACTACTCAGACCATCATCAGACGCTCTTGAACTGGCGGTCCCAATCACCCTC	242
QY	333	ILeTrpLeuIIePhePheTYrTrpLeuPheHisSerCYeLeuAlaAlaValAlaJuLeu	352
Db	243	ATCTGGCTCATCTTCTTCTACTGGCTCTTCCATCTCCGCTGAATGCGGGCTGAGCTC	302
QY	353	MetGlnPheGlyAspArgGJuPheTYrTrpAspTrpTrpAsnSerGJuSerValThiTYr	372
Db	303	ATGCAAGTTTGGAGACCGGAGGTTCTACCGGAGCTGGAGAACTCCGAGTGTGCACCTAC	362
QY	373	PheTrpGlnAsnTrpAsnIIeProValHisLYeTrpCYeIIeArgHisPheTYrLYsPro	392
Db	363	TTCTGGCAACACTGGAAACATCCCTGTGGCAACAATGGTGATTCAGACACTTCTACAAAGCC	422
QY	393	MetLeuAlaArgArgLYsSerSerLYsTrpMet	402
Db	423	ATGCTTCGACGGGGCGACGACAGTGTGAATG	452

RESULT 2

US-09-867-701-5894
; Sequence 5894, Application US/09867701

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: Patient No. US20020132237A1
: GENERAL INFORMATION:
: APPLICANT: Aglate, Paul A.
: APPLICANT: Jones, Robert
: APPLICANT: Harlockee, Susan L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF OVARIAN CANCER
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF OVARIAN CANCER
: FILE REFERENCE: 210121.497
: CURRENT APPLICATION NUMBER: US/09/867,701
: CURRENT FILING DATE: 2001-05-29
: NUMBER OF SEQ ID NOS: 10912
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5894
: LENGTH: 371
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-867-701-5894

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Alignment Scores:

Pred. No.:	6.86e-60	Length:	371
Score:	612.00	Matches:	133
Percent Similarity:	99.2%	Conservative:	0
Best Local Similarity:	99.2%	Mismatches:	1
Query Match:	23.6%	Indels:	1
DB:	3	Gaps:	0

US-10-659-800-6 (1-488) x US-09-867-701-5894 (1-371)

QY	186	ValGIuSerIeThrProValGIuSerLeuLeuAlaLeuMetAlaHisThrIleLeuPhe	205
Db	1	GTTCAGTCTATCACTCAGTGGGCTCCCTGGCGCTGATGAC-CACACATCCTCTTC	59
QY	206	LeuLysLeuPheSerTyraArgaspValamSerTyrCyaraArgmIaaGAlaLysAla	225
Db	60	CTCAAGCTTTCTCCCTAACCGCGACGTCMAATCAGTGGCGGACAGGGCCAGGGCCAAAGCT	119
QY	226	AlaSerAlaGIuLysIysAlaSerSerAlaAlaAlaProHisThrValSerTyrProAsp	245

Db	120	GCCTTGCAGGGANANAAGGCCAGCAGTGTCTGTGCCGACACACGTTAGTCACCCGGAC	179
Qy	246	AsnLeuThrTyrArgAspLeuTyrTyrPheLeuPheAlaProThrLeuCystrArgLeu	265
Db	180	AATCGACCTACCGGATCTCTACTACTTCTCTTCGCCCCACCTTGTGCTAACGAGCTC	239
Qy	266	AsnPheProArgSerProArgIleArgTysArgPheLeuLeuArgArgIleLeuGlnMet	285
Db	240	AACTTTCCCGCTCTCCCGCATCCGGAGGCCCTTCTCTCTCGACGAGATCTTGAGATG	299
Qy	286	LeuPhePheArgGlnLeuGlnValGlyLeuIleGlnGlnTyrMetValProThrIleGln	305
Db	300	CTGTTCTTCACCCACTCCAGGTGGGGCTGATCGACAGTGTATGATCCCAACATCCAG	359
Qy	306	AsnSerMetLys	309
Db	360	AACTCCATGAAG	371

RESULT 3

US-09-764-853-314
; Sequence 314, Application US/09764853

; Patent NO. US20020090672A1
; GENERAL INFORMATION:
;

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

```

; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853

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; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
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; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0.6; SEQ ID NO 314
; LENGTH: 433

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; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: SITE

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; LOCATION: (428
; OTHER INFORMAT

US-09-764-853-314

Alignment Scores:		
Pred. No.:	8.26e-59	Leng

Score:	603.50	Match
Percent Similarity:	87.2%	Cons

Best Local Similarity:	85.1%	Mismatches:
Query Match:	23.3%	Index:

DB:	3	Gaps:
-----	---	-------

US-10-659-800-6 (1-488) X US-09-764-853-314 (1-433)

QY 264 GULEuAnpHeProARgSerProARgIleArgLyARgPHeuLeuARgIleLeu 283

Db
1 GAGCTCACTTCCCGGCTCCCGGCATCCGGAAGCGCTTCTGTGGCAGGATCTT 60

284 GUMETLEUPhEhETInLeuclNValGlyLeuIleGInGInTryptMetValProThr 303

Db 61 GAGATGCTGTTCTTCAACCAGCTCCAGGTGGGGCTGATCCACAGTGGATGCTCCACC 120

304 IlegiaAsnSerMetLysProPheLysAspMetAspTyrSerArgIleIleGluArgLeu 323

Db 121 ATCCAGACTCCATGAGGCCCTTCAAGACACTGAGACTCAGCCATCATCGAGGCCCTC 180

```

324 LeuyluyluyluValProvlvnlvlleutlrllellleherheylutlrleurenlv 343

```

Db 181 CTGAAGCTGGCGGTCCCAATCACCATCATCTGGGTCATCTTCTACTGGCTCTTCAC 240

344 SercysuenaAlaValagilueuercInphe-GlyAspArgGlnphelyArgAs 363

241 TCCTGCTGATGCGTGGCTGACTCATTCAGTTGGGAGACCCGGAGTTCTACCCGGA 300

```

363 pTIPrIP-AonSeRCIuse-ValTrrTyRhe---TIpGInASnrrP-AaRIePVoI 381
||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||

```

```
Db 301 CTGGTGGGAATTCGAGTGTTCACCTAATTTCTGGGAGCACTGGGAACATCCCTGTG 360
Qy 382 -HislystPcysIleArg--HisPheTyrlYsPrometleuArgArgIyserserlyS 400
Db 361 GCACAGTGTGATTCACAGCAATTTTAAAGCCCAKGTTCCTTGAMGGGGGAGCAGCA 420
Qy 401 TTPMetAlaArg 404
Db 421 TTGATGCAGCAGG 432

RESULT 4
US-09-918-995-29256
; Sequence 29256; Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29256
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ..(447)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-29256

Alignment Scores:
Pred. No.: 1,32e-54 Length: 447
Score: 567.00 Matches: 107
Percent Similarity: 77.7% Conservative: 1
Best Local Similarity: 77.0% Mismatches: 0
Query Match: 21.9% Indels: 31
DB: Gaps: 2

US-10-659-800-6 (1-488) x US-09-918-995-29256 (1-447)

Qy 298 GINTP-----MetValProThrIleGlnAsnSerMetIysProPheIys----- 312
Db 31 CGGTGAATTCGCGAGATGTCCTCCCAACATCCATGAAAGCCCTTCAAGGGAGCT 90
Qy 312 ----- 312
Db 91 GGCTATGTCCTTTCGACGCTGGGCTGGGGAGTGAACCGAGACATGCTAGCTGAA 150
Qy 313 -----AspMetAspTyrSerArgIleIleGlnArgLeuLeuIysLeuAl 327
Db 151 GGGCTGTTCCTTCGAGGACATGACACTCAAGCATCAACGCGCTCTGAAGCTGCG 210
Qy 327 AValProAsnHisLeuIleTyrLeuIlePhePheTyrlYsLeuPheHisSerCysLeuAs 347
Db 211 GGTCCCAATCACCCTCATCTGCTCATCTTCTTACTAGGCTCTTCACTCCGCTGAA 270
Qy 347 nAlaValAlaGluMetGlnPheGlyAspArgGluPheTyrlYsAspTyrTPAsnSe 367
Db 271 TGCCTGTGCTGACCTTCATGACATTTGAGAACCGGAGTTCATCCGGAGCTGGTGAACCTC 330
Qy 367 rGluSerValThrTyrlYsPheTyrGlnAsnTyrPAsnIleProValHislystPcysIleAr 387
Db 331 CGAGCTGTGACCTTCTTCGACAGACTGGAACATCCCTGTGCAAGTGTGATCG 390
Qy 387 gHisPheTyrlYsPheMetLeuArgArgIyserserlySTrpMetAlaArgThr 405
Db 391 ACACTTCAACAGCCCATGCTTCGACGGGAGCAGCAAGTGAAGGCCAGACAA 445
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```
RESULT 5
US-10-741-600-12886
; Sequence 12886; Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12886
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-12886

Alignment Scores:
Pred. No.: 4.78e-33 Length: 201
Score: 374.00 Matches: 65
Percent Similarity: 98.5% Conservative: 0
Best Local Similarity: 98.5% Mismatches: 1
Query Match: 14.4% Indels: 0
DB: Gaps: 0

US-10-659-800-6 (1-488) x US-10-741-600-12886 (1-201)

Qy 346 LeuAsnAlaValAlaGluMetGlnPheGlyAspArgGluPheTyrlYsAspTyrTP 365
Db 3 CTGAATGCCGTGGCGAGCTATGACGTTTGAGACCGGGAGTTTACCGGACCTGGTG 62
Qy 366 AensergIuserValThrTyrlYsPheTyrGlnAsnTyrPAsnIleProValHislystPcys 385
Db 63 AACTCGAGTCGTACCTACTTCGGCAGAACTGGAASATCCCTGTGCACAAAGTGTGC 122
Qy 386 IleArgHisPheTyrlYsPrometleuArgArgIyserserlySTrpMetAlaArgThr 405
Db 123 ATCAGACACTTCTTACAGCCATGCTTCGACGGGAGCAGCAAGTGAAGTGCAGACA 182
Qy 406 GlyValPheLeuAlaSer 411
Db 183 GGGGTGTCTCGGCTCG 200
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RESULT 6
US-10-741-600-12898
; Sequence 12898; Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12898
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-12898

Alignment Scores:
Pred. No.: 4.78e-33 Length: 201
Score: 374.00 Matches: 65
Percent Similarity: 98.5% Conservative: 0
Best Local Similarity: 98.5% Mismatches: 1
Query Match: 14.4% Indels: 0
DB: Gaps: 0

US-10-659-800-6 (1-488) x US-10-741-600-12898 (1-201)
```

```
OY 346 LeuAenAlaValAlaGluLeuMetGlnPheGlyAspArgLysPheTyrArgAspTrpTrp 365
Db 3 CTGAATGCCGCTGAGCTCATGACGTTGGAGACGGGAGTTCTACCGGAGCTGGTG 62
OY 366 AenSerGluSerValThrTyrPheTrpGlnAenTrpAsnLysProValHisLysTrpCys 385
Db 63 AACTCCGAGTCTGTCACTTCTGGGAGAACTGGAAATATCCCTGTCACAAAGTGATCC 122
OY 386 IleArgHisPheTyrLysProMetLeuArgLysSerSerLysTrpMetLysArgThr 405
Db 123 ATCAGACACTTCTTACAGCCCATGCTTCACGCGGACAGCAGCAAGTGTGCGCAGACA 182
OY 406 GlyValPheLeuAlaSer 411
Db 183 GGGGCTGTTCTGGCTTCG 200

RESULT 7
US-09-918-995-1979
; Sequence 1979, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hybreg, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1979
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(471)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1979

Alignment Scores:
Pred. No.: 1.2e-27 Length: 471
Score: 332.00 Matches: 71
Percent Similarity: 53.4% Conservative: 0
Best Local Similarity: 53.4% Mismatches: 2
Query Match: 12.8% Indels: 62
DB: 3 Gaps: 2

US-10-659-800-6 (1-488) x US-09-918-995-1979 (1-471)
OY 315 AspTyrSerArgLysIleGluArgLeuLeuLysLeuAla----- 327
Db 58 GACTACTACGCGATCATCGAGCGCTCCGGAAGCTGGC-GGTGAGTGGCAGAGGTGGCG 116
OY 327 ----- 327
Db 117 CATGCACAGACAGAGGGGAGACGTGGCGAGGAAAGTTCTAGAACTTGTCGCCA 176
OY 328 -----ValProAsnHisLeuLysIleTrpLeuLysPhePheTyrTrpLeu 341
Db 177 CCCCACCTCCCTGCGAGGTCCCAATCATCTGCTCATCTTCTTCTTACAGGCTC 236
OY 342 PheHisSerCysLeuAsnAlaValAlaGluLeuMetGlnPheGlyAspArgLysPheTyr 361
Db 237 TTCACCTCCCTGCTGAATGCGCTGCTGAGCTCATGACGTTTGAGACCGGAGTTCTAC 296
OY 362 ArgAspTrpTrpAsn----- 366
Db 297 CGGAGCTGTGTGTG-AGTGTCCCTGGGGGTGTCCTGGGGGCTGGGAGTGGCCATGTGTG 355
OY 367 -----SerGluSerValThrTyrPheTrp 374
```

```
Db 356 CTGTGATCCCCGTGGTGGTCTGTGGCCCCCAGGAACCTCGAGTCTGTCACTTCTGG 415
OY 375 GlnAenTrpAsnLysProValHisLysTrpCysIleArg 387
Db 416 CAGAACTGGAACTATCCCTGTGACAAAGTGTGATCAGG 454

RESULT 8
US-09-770-791-192
; Sequence 192, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, Maja
; APPLICANT: Slader, Red
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurdan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(380)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-791-192

Alignment Scores:
Pred. No.: 1.27e-27 Length: 380
Score: 330.50 Matches: 60
Percent Similarity: 69.3% Conservative: 26
Best Local Similarity: 48.8% Mismatches: 34
Query Match: 12.7% Indels: 3
DB: 3 Gaps: 2

US-10-659-800-6 (1-488) x US-09-770-791-192 (1-380)
OY 273 IleArgLysArgPheLeuLeuArgArgLysLeuGluMetLeuPhePheThrGlnLeuGln 292
Db 16 ATACGGAAGGGTGGGTGGCTCGTCAATTTGCAGAAATGTCATATTCACCGGATTTCATG 75
OY 293 ValGlyLeuLysGlnGlnTrpMetValProThrLysGlnAsnSerMetLysProPheLys 312
Db 76 GGATTATATATAGAACATATATATATTCCTTGTTCAGGAATCAAGACATCTTGGAAA 135
OY 313 ---AspMetAspTyrSerArgLysIleGluArgLeuLeuLysLeuAlaValProAsnHis 331
Db 136 GCGCATCTTCTATATGCT-----ATTCAAGAGAGTTGAAAGCTTTCAGTTCGAAATTTA 189
OY 332 LeuLysTrpLeuLysPhePheTyrTrpLeuPheHisSerCysLeuAsnAlaValAlaGlu 351
```

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Db      190 TAATGCTGGCTTCGCAATGTTACTGCTCTTCACCTTGGTTAAACATATTGGCAGAG 249
Oy      352 LeuMetGlnPheGlyAspArgGluPheTyrArgAspTyrTyrAsnSerGluSerValThr 371
Db      250 CTTCTCTGCTGGGGGATCGTAATCTTCACAAAGATGGTGCAATCAAAAAGTGTGGGA 309
Oy      372 TTTPhetTgPAsnTyrPAsnIleProValHisIleTyrCysIleIleArgHisPheTyrLys 391
Db      310 GATTACTGGAGAAATGTGNNATGCTCTGTTCTAATTAATGATGGTTCGACATATTACTTC 369
Oy      392 ProMetLeu 394
Db      370 CGGTGCTTG 378

RESULT 9
US-10-741-600-12888
; Sequence 12888, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; NUMBER OF SEQ. ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12888
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-12888

```

```

Alignment Scores:
Pred. No.: 5,64e-27 Length: 201
Score: 321.00 Matches: 65
Percent Similarity: 98.5% Conservative: 1
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 12.4% Indels: 0
DB: 8 Gaps: 0

US-10-659-800-6 (1-488) x US-10-741-600-12888 (1-201)

Oy 119 GlnValValSerLeuPheLeuLysAppProHisSerTyrProAlaProCysLeuValIle 138
Db 1 CAGGGGGTTTCTCTGTCTCTGCTGAAGCATCTCCCTAGCTGGCCCGGCCAGGCTGTATT 60
Oy 139 AlAlaAenValPheAlaValAlaAlaPheGlnValGluLysArgLeuAlaValGlyAla 158
Db 61 GCGGCGCATGTCTTGTCTGTGGCTGATCCAGGTTGAGARGGCGCTGGCGGGGTGCC 120
Oy 159 LeuThrGluGlnAlaGlyLeuLeuLeuHisValAlaAenLeuAlaThrIleLeuCysPhe 178
Db 121 CTGAGGAGGACGAGCGGGAGCTGCTGCTGCACGTCGGCCAACTG6CCACCATCTGTGTTC 180
Oy 179 ProAlaAlaValAlaLeuLeu 185
Db 181 CCAGCGGCTGTGTCTTACTG 201

RESULT 10
US-10-741-600-12894
; Sequence 12894: Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FASTSEQ for Windows Version 4.0

```

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; SEQ ID NO 12894
;
; LENGTH: 201
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
US-10-741-600-12894

Alignment Scores:
Pred. No.:      5,64e-27      length:      201
Score:          321.00      Matches:      65
Percent Similarity: 98.5%      Conservative: 1
Best Local Similarity: 97.0%      Mismatches:  0
Query Match:    12.4%      Indels:      0
DB:             8          Gaps:
US-10-659-800-6 (1-488) x US-10-741-600-12894 (1-201)

```

US-10-659-800-6 (1-488) x US-10-741-600-12894 (1-201)

QY	119	GINValValSerIeuPheIeuYsaPheProHisSerTTPProAlaProCysIeuValIle	138
Db	1	CAGGTGGTTCCTCTGTTCCTGAAGATCCCTATAGCTGGCCGCCCATGCTGGTAAATT	60
QY	139	AlaIaAsnValPheAlaValAlaAlaPheGlnValGluYsaArgIeuAlaValAla	158
Db	61	GCGGCCCAATCTCTTCTGCTGGCTGCATTCCAGGTGAGAGCGCCCTGGCGGTGGCC	120
QY	159	LeuThrGlnGlnAlaGlyLeuIeuLeuHisValAlaAsnIeuAlaThrIleLeuCysPhe	178
Db	121	CTGACGGAGCAGCGGGAGCTGCTGCTGACGTCGCGCAACTGGCCACCATTCCTGTGTTTC	180
QY	179	ProAlaIaValValIeuIeu	185
Db	181	CCAGCGGCTGTGGTCTTACTG	201

```

RESULT 11
US-10-741-600-12900
; Sequence 12900, Application US/10741600
; Publication NO. US20050026169n1
; GENERAL INFORMATION:
; APPLICANT: CARGLL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12900
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-12900

Alignment Scores:
Pred. No.: 5,64e-27 Length: 201
Score: 321.00 Matches: 65
Percent Similarity: 98.5% Conservative: 1
Best Local Similarity: 97.0% Mismatches: 1
Query Match: 12.4% Indels: 0
DB: 8 Gaps: 0

US-10-659-800-6 (1-488) x US-10-741-600-12900 (1-201)

QY 119 GlnValValIsSerLeuPheLeuLysAspPrhIIsSerTIPProAlaProCysLeuValIle 138
Db 1 CAGGtGGtTTCtCTGtTTCCTGAGGATcCCTATAGctGGCCGcCCcCATGcCTGgTtATt 60

QY 139 AlaAlaenValPheAlaValAlaAlaPheGlnValGluYbArgLeuAlaValGlyAla 158
Db 61 GCGGcCATATGcCTTtGCTGCTGCTGcCATtTCcAGGTtTGAGARcCGcCTGcGGTGGtGCC 120

QY 159 LeuThrGlnGlnAlaGlyLeuLeuLeuHrIsvAlaAlaenLeuAlaThrIleLeuCysPhe 178
Db 121 CTGACGAGcAGcGGcGGGAcCTcTcTcTcGAcTcGcCAcTtGcCCAcCTtGcCCAcCATtCTGtGtTTC 180

```

QY 179 ProAlaAlaValIleuLeu 185
|||
Db 181 CCAAGCGCTGTGCTTACTG 201

RESULT 12

US-10-741-600-12905
; Sequence 12905, Application US/10741600
; Publication No. US20050026169A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12905

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens

US-10-741-600-12905

Alignment Scores:

Pred. No.:	5,646-27	Length:	201
Score:	321.00	Matches:	65
Percent Similarity:	98.5%	Conservative:	1
Best Local Similarity:	97.0%	Mismatches:	1
Query Match:	12.4%	Indels:	0
	8	Gaps:	0

US-10-659-800-6 (1-488) x US-10-741-600-12905 (1-201)

QY 119 GlnValSerLeuPheLeuYAspProHisSerProAlaProCysIleuValIle 138
|||
Db 1 CAGGGGTTTCTCTCTCTGTAAGATCCCTTACTGCGCCGCCCATGCTGTATT 60

QY 139 AlaAlaenValPheAlaValAlaAlaPheGlnValGluLeuArgLeuAlaValAla 158
|||
Db 61 GCGGCCAATGTTTCTGCTGTGCTGCTCATTCAGGTTGAGACGCCCTGCGGTGCC 120

QY 159 LeuThrgJugAlaGlyLeuLeuLeuHisValAlaAsnLeuAlaThrIleLeuCysPhe 178
|||
Db 121 CTGAGCGAGCAAGCGGACGCTGCTGCGACGTCGCAACCTGCGCACCATCTGTGTTTC 180

QY 179 ProAlaAlaValIleuLeu 185
|||
Db 181 CCAAGCGCTGTGCTTACTG 201

QY 181 CCAAGCGCTGTGCTTACTG 201

RESULT 13

US-10-424-599-115051
; Sequence 115051, Application US/10424599
; Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 115051

LENGTH: 362

TYPE: DNA

ORGANISM: Glycine max

FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_74900C.1

US-10-424-599-115051

Alignment Scores:

Pred. No.:	4,496-23	Length:	362
Score:	290.50	Matches:	55
Percent Similarity:	73.9%	Conservative:	30
Best Local Similarity:	47.8%	Mismatches:	27
Query Match:	11.2%	Indels:	3
	7	Gaps:	2

US-10-659-800-6 (1-488) x US-10-424-599-115051 (1-362)

QY 247 LeuThrYrArgAspLeuTyrPheLeuPheAlaProHisLeuCysTyrGluLeuAsn 266
|||
Db 22 GFAACCTCAAGAGCTTGCATATTCTGTGTCCTCACTTATGTTTACCAAGCAAGC 81

QY 267 PheProArgSerProArgIleArgIleYAspPheLeuLeuArgArgIleLeuGluMetLeu 286
|||
Db 82 TATCTCCACACCTTATATTCGAAGGGCTGGCTTCCCAACTGTCAAGCTGATA 141

QY 287 PhePheThrgInLeuGlnValGlyLeuIleGlnIntrPheValProThrIleGlnAsn 306
|||
Db 142 ATATTACAGAGATTATGGATTATATACACATCATTAATCCCATTTGACAAAT 201

QY 307 SerMetCysPropPheLeu--AspMetAspTyrSerArgIleIleGluArgLeuLeuYs 325
|||
Db 202 TCACAGCATCTCTCAAGGAAACCTTCTTACGCC-----ATCGAGAGATTCTGAAG 255

QY 326 LeuAlaValProAsnHisLeuIleTyrPheLeuPhePheTyrTrpLeuPheHisSerCys 345
|||
Db 256 CTTTCTGTCCAAATTTATGTGTGGCTCGCATGTTCTATTGCTTTTCCACCTTTGG 315

QY 346 LeuAsnAlaValAlaGluLeuMetGlnPheGluYAspArgGluPhe 360
|||
Db 316 TTAATATATATGGCAGAGCTTCTTCGATTTGTGTATCGTAATTC 360

QY 316 TTAATATATATGGCAGAGCTTCTTCGATTTGTGTATCGTAATTC 360

QY 316 TTAATATATATGGCAGAGCTTCTTCGATTTGTGTATCGTAATTC 360

RESULT 14

US-10-741-600-12887
; Sequence 12887, Application US/10741600
; Publication No. US20050026169A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12887

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens

US-10-741-600-12887

Alignment Scores:

Pred. No.:	3,416-23	Length:	201
Score:	288.00	Matches:	54
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.1%	Indels:	0
	8	Gaps:	0

US-10-659-800-6 (1-488) x US-10-741-600-12887 (1-201)

QY 435 MetAlaGlnIleProLeuAlaTrpPheValGlyArgPhePheGlnGlyAsnTyrGlyAsn 454
|||
Db 3 ATGGCTCAGATCCCACTGCTGCTGTGCGCGCTTTTCCAGGGCACTATGGCAAC 62

QY 455 AlaAlaValTrpLeuSerLeuIleIleGlyGlnProIleAlaValLeuMetTyrValHis 474
|||
Db 63 GCAAGTGTGTGGCTGTGCTCATCATCGACAGCAATWGCCTCATGTATGATCTCAC 122

QY 475 AspTyrTyrValLeuAsnTyrGluAlaProAlaAlaGluAla 488
|||
Db 123 GACTACTAGTGTCTCAACTATGAGGCCCAAGCGGAGAGGCC 164

QY 123 GACTACTAGTGTCTCAACTATGAGGCCCAAGCGGAGAGGCC 164

Tue May 9 11:43:30 2006

RESULT 15

US-10-741-600-12893
 ; Sequence 12893, Application US/10741600
 ; Publication No. US20050026169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C0001499
 ; CURRENT APPLICATION NUMBER: US/10/741,600
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 73997
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12893
 ; LENGTH: 201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-741-600-12893

Alignment Scores:

Pred. No.:	3,41e-23	Length:	201
Score:	288.00	Matches:	54
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	11.1%	Indels:	0
DB:	8	Gaps:	0

US-10-659-800-6 (1-488) x US-10-741-600-12893 (1-201)

QY 435 MetAlaGlnIleProLeuAlaTrpPheValGlyArgPheGlnGlyAsnTrpGlyAsn 454
 DB 3 ATGGCTCAGATCCCACTGGCTGGTTCCGTGGCCGCTTTTCCAGGGCAACTATGGCAAC 62
 QY 455 AlaAlaValTrpLeuSerLeuIleIleGlyGlnProIleAlaValLeuMetTrpValHis 474
 DB 63 GCAGCTGTGTGGCTGTGGCTCATCATCGGACAGCCAAATGCGTCTCATGTACGTCCAC 122
 QY 475 AspTrpTrpValLeuAsnTrpGlnAlaProAlaAlaGlnAla 488
 DB 123 GACTACTACGTGCTCACTATGAGGCCCGCGGCGAGAGGCC 164

Search completed: May 7, 2006, 03:28:27
 Job time : 1157 Secs

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GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 6, 2006, 12:03:36 ; Search time 378 Seconds
(without alignments)
3442.262 Million cell updates/sec

Title: us-10-659-800-6
Perfect score: 2594
Sequence: 1 MGDGSSRRRTGSRPSHG.....VLMVHYDYVINYEAFAEA 488

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 1790828

Minimum DB seq length: 0
Maximum DB seq length: 500
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-O=/abs/ABSSWB_spool/US10659800/runat_05052006.122310.17268/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.szlm500.rn1 -MINMATCH=0.1
-LOOFC1=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=spc -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=500 -HOST=abs602p
-USER=US10659800@CGN1_1.512@runat_05052006.122310.17268 -NCPU=6 -ICPU=3
-NO MMAP -NCG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEX=7

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCITUS_COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	232	8.9	299	3	US-09-326-203A-13
2	197.5	7.6	381	3	US-09-326-203A-20
3	176	6.8	113	3	US-09-621-976-14231
4	170	6.6	275	3	US-09-326-203A-5
5	164	6.3	225	3	US-09-172-711-58
6	155	6.0	253	3	US-09-326-203A-7
7	127	4.9	267	3	US-09-326-203A-4
8	123.5	4.8	234	3	US-09-326-203A-3

9	103	4.0	200	3	US-09-533-559-1684	Sequence 1684, Ap
10	91	3.5	447	3	US-09-252-991A-292	Sequence 292, App
11	89.5	3.5	325	3	US-09-326-203A-10	Sequence 10, Appl
12	88.5	3.4	453	3	US-09-252-991A-11268	Sequence 11268, A
13	88.5	3.4	465	3	US-09-252-991A-8944	Sequence 8944, Ap
14	88.5	3.4	485	3	US-09-270-767-10793	Sequence 10793, A
15	88	3.4	257	3	US-09-326-203A-6	Sequence 6, Appl1
16	88	3.4	420	3	US-09-902-540-5709	Sequence 5709, Ap
17	87.5	3.4	419	3	US-09-270-767-26258	Sequence 26258, A
18	87	3.4	405	3	US-09-252-991A-7771	Sequence 7771, Ap
19	87	3.4	462	3	US-09-902-540-7093	Sequence 7093, Ap
20	86	3.3	354	3	US-09-252-991A-7022	Sequence 7022, Ap
21	85	3.3	369	3	US-09-902-540-8920	Sequence 8920, Ap
22	83	3.2	405	3	US-09-902-540-5868	Sequence 5868, Ap
23	82	3.2	496	3	US-09-854-133-495	Sequence 495, App
24	81.5	3.1	482	3	US-09-902-540-6395	Sequence 6395, Ap
25	81	3.1	429	3	US-09-489-039A-1628	Sequence 1628, Ap
26	80.5	3.1	429	3	US-09-252-991A-6653	Sequence 6653, Ap
27	80	3.1	312	3	US-09-902-540-5352	Sequence 5352, Ap
28	80	3.1	420	3	US-09-252-991A-4348	Sequence 4348, Ap
29	80	3.1	441	3	US-08-914-375C-51	Sequence 51, Appl
30	80	3.1	486	3	US-09-252-991A-1276	Sequence 1276, Ap
31	79.5	3.1	418	3	US-10-131-827-8386	Sequence 8386, Ap
32	79.5	3.1	423	3	US-09-854-133-713	Sequence 713, App
33	79	3.0	435	3	US-08-692-922-3	Sequence 3, Appl1
34	79	3.0	465	3	US-09-252-991A-15919	Sequence 15919, A
35	79	3.0	483	3	US-09-902-540-1856	Sequence 1856, Ap
36	78.5	3.0	464	2	US-08-718-538-6	Sequence 6, Appl1
37	78	3.0	372	3	US-09-513-999C-17335	Sequence 17335, A
38	78	3.0	326	3	US-09-902-540-8592	Sequence 8592, Ap
39	78	3.0	479	2	US-08-757-541-6	Sequence 6, Appl1
40	78	3.0	479	3	US-09-033-275-6	Sequence 6, Appl1
41	78	3.0	479	3	US-09-342-581-6	Sequence 6, Appl1
42	77.5	3.0	285	3	US-09-902-540-9636	Sequence 9636, Ap
43	77.5	3.0	402	3	US-09-252-991A-10958	Sequence 10958, A
44	77.5	3.0	438	3	US-09-252-991A-3849	Sequence 3849, Ap
45	77	3.0	269	3	US-09-313-294A-115	Sequence 115, App

ALIGNMENTS

RESULT 1
US-09-326-203A-13
; Sequence 13, Application US/09326203A
; Patent No. 6444876
; GENERAL INFORMATION:
; APPLICANT: Laesner, Mike
; TITLE OF INVENTION: Ruezinkv, Diane
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; FILE REFERENCE: 17045/00/NO
; CURRENT APPLICATION NUMBER: US/09/326,203A
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 299
; TYPE: DNA
; ORGANISM: murine
US-09-326-203A-13

Alignment Scores:
Pred. No.: 2.77e-15
Score: 232.00
Percent Similarity: 96.1%
Best Local Similarity: 86.3%
Query Match: 8.9%
DB: 3
Length: 299
Matches: 44
Conservative: 5
Mismatch: 2
Indels: 1
Gaps: 0

```
US-10-659-800-6 (1-488) x US-09-326-203A-13 (1-299)
Qy 434 MetwetaIaGlnIleProleuAlaTrpPheValGlyArpPhehngInglYAsnTYrGly 453
Db 3 ATGATGGCTCAGTCCAGCTGCGCTGGATTTGGGCGCCGATTTTCAGAGGAACTATGGC 62
Qy 454 AsnAlaValaTrpLeuSerLeuIleIleGlyGlnProIleAlaValLeuMetTYrVal 473
Db 63 AATGAGCTGTGTGGTGACACTCATTCATTGGGCAACGGGTGCTGT-CTCATGTATATGC 121
Qy 474 HisApTYrTYrValLeuAsnTYrGlnAlaPro 484
Db 122 CACGACTACTAGTCTCACTCACTACATGATGCCCA 154

RESULT 2
US-09-326-203A-20
; Sequence 20, Application US/09326203A
; Patent No. 6444876
; GENERAL INFORMATION:
; APPLICANT: Laesener, Mike
; APPLICANT: Ruzsineky, Diane
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; FILE REFERENCE: 17045/00/WO
; CURRENT APPLICATION NUMBER: US/09/326,203A
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (46)
; OTHER INFORMATION: n at position 46 is unknown
US-09-326-203A-20

Alignment Scores:
Pred. No.: 1,75e-11 Length: 381
Score: 197.50 Matches: 41
Percent Similarity: 61.2% Conservative: 22
Best Local Similarity: 39.8% Mismatches: 31
Query Match: 7.6% Indels: 9
DB: 3 Gaps: 2

US-10-659-800-6 (1-488) x US-09-326-203A-20 (1-381)
Qy 47 PrcdAlaProAlaProAsn-----LysAspGlyAspAlaGlyValGly 60
Db 71 CCAGTAGACGCTCCCTCATTTGGCAAAATGTAAATTCGCAAGGAAATTCAGAAATG 130
Qy 61 SerGlyHsTrpGlnLeuArgCysHisArgLeuGlnAspSerLeuPheSerAspSer 80
Db 131 AGAGGACCTGGGCAAAAGTGTACACTGCTCAAGATTCATTGTTTCCAGCGATTC 190
Qy 81 GlyPheSerAsnTYrArgGlyIleLeuAsnTrpCysValValMetLeuIleLeuSerAsn 100
Db 191 GGATGGACAAATTTCTCGTGAATTTCTCAATTTGCTAATTTTCTTTGGTACTTCAAT 250
Qy 101 AlaArgLeuPheLeuGlnAsnLeuIleLeuTYrGlyIleLeuValAspProIleGlnVal 120
Db 251 GGAGCGCGGCGCACTTGAAATGTGTATCAAAATATGATTTTGATACACCCCTTCAGTGG 310
Qy 121 ValSerLeuPheLeuLeuAspProHis-----SerTrpProAlaProCysLeuVal 137
Db 311 ATCTCAACGTTTGTGGACATCATTCAATTGGAGCTGGCAAAATCTGCTCTCATC 370
Qy 138 IleAlaAla 140
```

```
Db 371 CTATGCTCA 379

RESULT 3
US-09-621-976-14231
; Sequence 14231, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14231
; LENGTH: 113
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14231

Alignment Scores:
Pred. No.: 4,35e-10 Length: 113
Score: 176.00 Matches: 36
Percent Similarity: 97.3% Conservative: 0
Best Local Similarity: 97.3% Mismatches: 1
Query Match: 6.8% Indels: 1
DB: 3 Gaps: 0

US-10-659-800-6 (1-488) x US-09-621-976-14231 (1-113)
Qy 417 TyrLeuValSerValProleuArgMetPheArgLeuTrpAlaPheTrnGlyMetMetAla 436
Db 3 TACCTGTGAGCGTCCTCTTCGAAATGTTCCGCTCTGGGG-TTCACGGGCAATATGGCT 61
Qy 437 GlnIleProleuAlaTrpPheValGlyArpPhehngInglYAsnTYrGly 453
Db 62 CAGATCCACACTGGCTGTGTGCGGCGCTTTTCCAGGCACTATGGC 112

RESULT 4
US-09-326-203A-5
; Sequence 5, Application US/09326203A
; Patent No. 6444876
; GENERAL INFORMATION:
; APPLICANT: Laesener, Mike
; APPLICANT: Ruzsineky, Diane
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; FILE REFERENCE: 17045/00/WO
; CURRENT APPLICATION NUMBER: US/09/326,203A
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (192..(263)
; OTHER INFORMATION: n at positions 192, 202, 204, 211, 222, 234, 238,
; OTHER INFORMATION: 239, 244, 245, 247, 251, 262, and 263 is unknown
US-09-326-203A-5

Alignment Scores:
Pred. No.: 8.01e-09 Length: 275
Score: 170.00 Matches: 34
```

Percent Similarity: 62.7% Conservative: 13
Best Local Similarity: 45.3% Mismatches: 28
Query Match: 6.6% Indels: 1
DB: 3 Gaps: 0

US-10-659-800-6 (1-488) x US-09-326-203A-5 (1-275)

Qy 365 TPASenSergluserValThrTyPheTyrGlnAsnTyrPAsnIleProValHisTyrTrp 384
Db 2 TCGAATGCCAAACCTTTCAGATATTCGAGAGTGAATATGCTTTCACAAATG 61
Qy 365 CysIleArgHisPheTyrIleProMetLeuArgArgIleSerSerIleTyrMetAlaArg 404
Db 62 ATGATCCGCCACCTATATTTTCATGTTAAAGCAGGATACCAAGCCGTTGCTT 121
Qy 405 ThrGlyValPheLeuAlaSerAlaPhePheHisGluTyrLeuValSerValProLeuArg 424
Db 122 TTAATTCCTTCCTGCTGT-CTGCTTATTCATGAGCTGTGATCGCTGTTCTTCCCA 180
Qy 425 MetPheArgLeuTyrAlaPheThrGlyMetMetAlaGlnIlePro 439
Db 181 CATATTCAGTNGTGGGTTTCNGNGAATTAGTTTCAGTTCCT 225

RESULT 5

US-09-172-711-58
Sequence 58, Application US/09172711
Patent No. 6160105

GENERAL INFORMATION:

APPLICANT: Cunningham, Mary Jane
APPLICANT: Zweigler, Gary B.

APPLICANT: Panzer, Scott R.
APPLICANT: Selhammer, Jeffrey J.

TITLE OF INVENTION: MONITORING TOXICOLOGICAL RESPONSES
FILE REFERENCE: PA-0011 US

CURRENT APPLICATION NUMBER: US/09/172,711
CURRENT FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL Program

SEQ ID NO 58
LENGTH: 225

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: unsure

LOCATION: 28, 59, 65, 73, 79, 84, 88
OTHER INFORMATION: a or g or c or t, unknown, or other

FEATURE: -
OTHER INFORMATION: 700627089H1

US-09-172-711-58

Alignment Scores:

Pred. No.: 2,466-08 Length: 225

Score: 164.00 Matches: 34

Percent Similarity: 83.0% Conservative: 5

Best Local Similarity: 72.3% Mismatches: 2

Query Match: 6.3% Indels: 6

DB: 3 Gaps: 1

US-10-659-800-6 (1-488) x US-09-172-711-58 (1-225)

Qy 184 LeuLeuValGluSerIleThrProValGlySerLeuLeuAlaLeuMetAlaHisThrIle 203
Db 85 TTANAGCTTGAGTCACTCACTCCAGTGGTTCCTGCTTCTTGGCATCACTCCATC 144

Qy 204 LeuPheLeuValLeuPheSerTyrArgAlaValAlaSerTyrCys-----ArgArgAla 221
Db 145 ATCTTCCTCAAGCTTTCTCCCTACCGGATGTCATCTGTGTGCGCCAGGAAAGGTC 204

Qy 222 ArgAlaValAlaAlaSerAla 228
Db 205 AAGGCCAAGCTGTGTGTGCA 225

RESULT 6

US-09-326-203A-7
Sequence 7, Application US/09326203A
Patent No. 6444876

GENERAL INFORMATION:

APPLICANT: Laesener, Mike

APPLICANT: Ruzinskiy, Diane

TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
FILE REFERENCE: 17045/00/MO

CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04

PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-11-12

NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7
LENGTH: 253

TYPE: DNA

ORGANISM: Zea mays

US-09-326-203A-7

Alignment Scores:

Pred. No.: 2,646-07 Length: 253

Score: 155.00 Matches: 36

Percent Similarity: 57.6% Conservative: 13

Best Local Similarity: 42.4% Mismatches: 31

Query Match: 6.0% Indels: 6

DB: 3 Gaps: 1

US-10-659-800-6 (1-488) x US-09-326-203A-7 (1-253)

Qy 375 GlnAsnTPASenIleProValHisTyrTrpCysIleArgHisPheTyrIleProMetLeu 394
Db 1 AGAAATGGAACATGCCCTGTCATMAATGATGTTCATCAATATATTTCTTGCAAG 60

Qy 395 ArgArgGlySerSerIleTyrMetAlaArgThrGlyValPheLeuAlaSerAlaPhePhe 414
Db 61 CGAATGATATATCAAGAGAGTTCCTGT-TTTATATCGTTCCTGTTCTGCTACTT 119

Qy 415 HisGluTyrLeuValSerValProLeuArgMetPheArgLeuTyrAla-PheThrGlyMet 434
Db 120 CATGATATATGATGTTGCTGTTCCCTGCCACATACATGTTCTGGGCTTTTATGAGAT 179

Qy 434 tMetAlaGlnIleProLeu-----AlaTyrPheValGlyArgPhePheGlnG 450
Db 180 CATGCTTCAGATTCCTCCCTCATCATATTCATCATCACTCAAAAATTAATTCAGTGAC 239

Qy 450 yAsnTyrGlyAsn 454
Db 240 AATGCTTGCAAT 252

RESULT 7

US-09-326-203A-4
Sequence 4, Application US/09326203A
Patent No. 6444876

GENERAL INFORMATION:

APPLICANT: Laesener, Mike

APPLICANT: Ruzinskiy, Diane

TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
FILE REFERENCE: 17045/00/MO

CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04

PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-11-12

NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4
LENGTH: 267

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; TYPE: DNA
; ORGANISM: Glycine max
US-09-326-203A-4

```

Alignment Scores:	0.000254	Length:	267
Pred. No.:	127.00	Matches:	32
Score:	57.6%	Conservative:	21
Percent Similarity:	34.8%	Mismatches:	31
Best Local Similarity:	4.9%	Indels:	9
Query Match:	3	Gaps:	3
DB:			

US-10-659-800-6 (1-488) x US-09-326-203A-4 (1-267)

Oy		ValGILSerLeuLeuLalaLeuLalashTIRLIleuPheLeuLeuPheSerTyr	211
Db		9 GTATTCGGGTCAACGTTGAATGCTATTAACTTGATGTGTGTTAAAATTGGTGCATAT	68
Oy		212 ArgAspValaIasnSerTrpCysArgAlaArgAlaValaIaLaIaSerAlaGlyLysLys	231
Db		69 GCACATACAAAC---TATGATATAGAGACACTTACTGTTGGATGAAAGAGAGA--	122
Oy		232 AlaSerSeraIaIaIaProHisThrValSer-----TyrProAsnLeuThaTyr	249
Db		123 -----ACATTCCCAATATTGTGAT-ATGAGATATCGGTACACTGTAACCTTC	169
Oy		250 ArgAspLeuTyrtYrPheLeuPheAlaProThrLeuCysTyrGluLeuAsnPheProArg	269
Db		170 AGAAGTTTGGCAACTTCATTCATGGTGTCTCTCAATTATGCTATACAGAACGTATCTCGC	229
Oy		270 SerProArgIleArgLysArPheLeuLeuArgArg	281
Db		230 ACACCTTCAGTTCGAAAGGGTTGGGCTTTCCTCA	265

RESULT 8
US-09-32

```

US-09-326-203A-3
: Sequence 3, Application US/09326203A
: Patent No. 6444876
:
: GENERAL INFORMATION:
: APPLICANT: Laesner, Mike
: APPLICANT: Ruzinskiy, Diane
: TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
: TITLE OF INVENTION: Acid Sequences
: FILE REFERENCE: 17045/00/MO
: CURRENT APPLICATION NUMBER: US/09/326,203A
: PRIOR APPLICATION NUMBER: 60/088,143
: PRIOR FILING DATE: 1998-06-05
: PRIOR APPLICATION NUMBER: 60/108,389
: PRIOR FILING DATE: 1998-11-12
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
:
: LENGTH: 234
:
: TYPE: DNA
: ORGANISM: Glycine max
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (24)..(60)
: OTHER INFORMATION: n at positions 24, 41, and 60 is unknown
:
: US-09-326-203A-3

```

Alignment Scores:

Pred. No.:	0.000478	Length:	234
Score:	123.50	Matches:	32
Percent Similarity:	67.9%	Conservative:	23
Best local Similarity:	39.5%	Mismatches:	22
Query Match:	4.8%	Indels:	5
DB:	3	Gaps:	2

US-10-659-800-6 (1-488) x US-09-326-203A-3 (1-234)

247 LeuThrTrpArgAspLeuTyrTrpPheLeuPheAlaPro-ThrLeuCysTyrGluLeuAs 266

Db	1	CTAGAGCTTCAAGAGCTTAGACATANTTCTCGTGGTGCCCTTANCAATTATGTTACCGCAAN	60
Qy	266	nphpeProlaGserProhrglllearglyaargPheleuleuLeargrarglleleuGmetle	286
Db	61	CTATCTCGACACACTTATATCGAAAGGGTTGGCTGTTGCCCAACTGT-CAACTGAT	119
Qy	286	uphePhehrginLeuginValglyLeuileglnGlnTrpMetValProThrllleGlnas	306
Db	120	AAATTTTACAGAGATTATGATGATTATATATAGAACATACATATATCCCATTTGACAAAA	179
Qy	306	nsrMetclpPropohelys--AspMetAspTysrargllelleGlnurgleuleuLy	325
Db	180	TTACACGACATCTCTTCACAGGAACACTTCTTACGCC-----ATCGAGAGAGTTCTGAA	233
Qy	325	p 325	
Db	234	G 234	

RESULT 9

```

US-09-533-559-1684
: Sequence 1684, Application US/09533559
: Patent No. 6902887
: GENERAL INFORMATION:
: APPLICANT: Randy M. Berka
: APPLICANT: Michael W. Rey
: APPLICANT: Jeffrey R. Shuster
: APPLICANT: Sakari Kauppinen
: APPLICANT: Ib Groch Clausen
: APPLICANT: Peter Bjarke Olsen
: TITLE OF INVENTION: Methods For Monitoring Multiple Gene
: TITLE OF INVENTION: Expression
: FILE REFERENCE: 5849, 200-US
: CURRENT APPLICATION NUMBER: US/09/533,559
: CURRENT FILING DATE: 2000-03-22
: EARLIER APPLICATION NUMBER: 09/273,623
: EARLIER FILING DATE: 1999-03-22
: NUMBER OF SEQ ID NOS: 7860
: SOFTWARE: FASTSeq for Windows Version 4.0
: SEQ ID NO 1684
: LENGTH: 200
: TYPE: DNA
: ORGANISM: Fusarium venenatum
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1)...(200)
: OTHER INFORMATION: n = A,T,C or G
US-09-533-559-1684

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Alignment Scores:

Pred. No.:	0.0529	Length:	2009
Score:	103.00	Matches:	26
Percent Similarity:	52.6%	Conservative:	14
Best Local Similarity:	34.2%	Mismatches:	25
Query Match:	4.0%	Indels:	11
DB:	3	Gaps:	1

US-10-659-800-6 (1-488) X US-09-533-559-1684 (1-200)

```

QY      213  ARGARGALANRGLALYALALASERLALGLYBLYSALASERLALALALAPRO 238
           |||||
DB      3  AGGAGAGCTCGAGCT-----TGTCCCGAGCTGTA 32

QY      239  HASTHVAL-SERYTPROASPENLTHRTYRARGASPLEUITYRPHLEUPHEAL 258
           |||||
DB      33  CACGCAATGCCCCGTATCCAGAAACATCACCTTTAGCAACCTGCCTATTTCGTGGTGGGC 92

QY      258  APTQTHLEUCSYTRGLULEAENPHEPRAISERPROARGILEARGLYSARGPHELE 278
           |||||
DB      93  ACCCAGGCTCATCTACCAAGCTGTGTATCCGACCAAAATNAAATGGGGTTTG 152

QY      278  ULEUARGATGLEUGLUMETLEUPHEPHERTHGLINLEUINAL 293
           |||||

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Db      153 GGGCCAAAGCGTGTGGAGAGACTTTGGCTCAAGGATTTCAATTG 198

RESULT 10
US-09-252-991A-292/c
; Sequence 292, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUDINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 292
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-292

Alignment Scores:
Pred. NO.:      3.62      Length:      447
Score:          91.00     Matches:      29
Percent Similarity: 44.0%   Conservative: 4
Best Local Similarity: 38.7% Mismatches:    36
Query Match:     3.5%      Indels:      6
DB:              3        Gaps:      3

US-10-659-800-6 (1-488) x US-09-252-991A-292 (1-447)

QY      1 MetGLyAspArgGLySerSerArgAlaArgAlaGhr-----GlySerArgProSer 17
Db      429 CTGGGTATTCGGGCATCTCCGACGAGCGCCGCAACTGTTCCGAGAGAGCGGCGCTGCC 370
QY      18 SerHisGLyGLyGLyGLyProAlaAlaAlaGluGluGluValAlaArgAlaAlaAlaGLy 37
Db      369 GCT---GGAGATGGGTGGCTGCAACTGTGCGGACCGAATTTTCAGCCAGCGCGCTGCCGGG 313
QY      38 ProAspValGLy-----AlaAlaGLyAspAlaProAlaProAlaProAlaValAspGLy 55
Db      312 CGCGCAACGAGTCGCGCGGCTCAAGCGCGCGCGCGCGCGATCCTGCGGAGCGAGCGGCTGGT 253
QY      56 AspAlaGLyValGLySerGLyHisIleProGluLeuArgCysHisArg 70
Db      252 GCGCGCGGGCGGTGACGTGCACAGAGGTGGTGCAGCAACTGATCGC 208

RESULT 11
US-09-326-203A-10
; Sequence 10, Application US/09326203A
; Patent No. 6444876
; GENERAL INFORMATION:
; APPLICANT: Laessner, Mike
; APPLICANT: Ruzizinsky, Diane
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; TITLE OF INVENTION: Acid Sequences
; FILE REFERENCE: 17045/00/WO
; CURRENT APPLICATION NUMBER: US/09/326,203A
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 10
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:

```

[illegible]

Oy	24	ProAlaIaaIaaIagLuGIuValAArgAspLaIaaIaa-----	36
Db	261	GAAAGGACGAGCCGGCGATGA---CTGCCTGCGCATGAACCAACATCCGCCA	314
Oy	37	----GlyProAspValGly-----AlaIaGlyAspAla---ProAla	48
Db	315	CTTCGGCAGAAGGCCAGAACCGAAGATCACCCCTGCGCGCGGCAAGACAACCTTGCA	374
Oy	49	ProAlaPProAnLysAsp-----GlyAspAlaGlyValGlySerGly	62
Db	375	ACTCCTGTGGTGGCGACAAACACATGTCCTGTAAGCGCACCTGTGGAGTGTGGAAAGAT	434
Oy	63	H ¹⁸ A 63	
Db	435	CAC 437	

```

RESULT 13
US-09-252-991A-8944
; Sequence 8944, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCES: 107196,136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8944
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8944

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Alignment Scores:	
Pred. No.:	7.08
Score:	86.50
Percent Similarity:	44.1%
Best Local Similarity:	38.2%
Query Match:	3.4%
DB:	3
	Gaps: 2
	Length: 465
	Matches: 26
	Conservative: 4
	Mismatches: 29
	Indels: 3
	Gaps: 2

US-10-659-800-6 (1-488) x US-09-252-991A-8944 (1-465)

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OY      4 ArgGlySerSerArgArgArgAlrghTrgIySerArgProSerSerHnAGLy----- 20
Db      235 AGATCATCGCAACCGCGGGTGGAACTTCCTCCACCACTGCATCTTTGTAAAGCGCCT 234
OY      21 -----GlyGlyGlyProAlaAlaAlaGluGluValuValArgAspAlaAla 35
Db      225 GTCCCTCTCCGCCCGGGAAGGAACTTGCGCCACTCCCCACTGTGCCGACGGCAGCA 354
OY      295 AlagIyProAspValGlyAlaAlaGlyAspAlaProAlaProAla---ProAenLysAsp 54
Db      36 |||||AlaGlyProAspValGlyAlaAlaGlyAspAlaProAlaProAla---ProAenLysAsp 54
OY      355 GCGCGGCAACAGGCTGCGCCGCCCGACAACCTCTGTGCGCGCAACC CGCAAC CAG 414
Db      35 |||||GCGCGGCAACAGGCTGCGCCGCCCGACAACCTCTGTGCGCGCAACC CGCAAC CAG 414
OY      55 GlyAspAlaGlyValGlySerGly 62
Db      415 TGACCTGCGCGGGTGGCACAGGC 438
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RESULT 14
US-09-270-767-10793/c
; Sequence 10793, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094

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? CURRENT APPLICATION NUMBER: US/09/270,766
? CURRENT FILING DATE: 1999-03-17
? NUMBER OF SEQ ID NOS: 62517
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 10793
? LENGTH: 485
? TYPE: DNA
? ORGANISM: Drosophila melanogaster
US-09-270-767-10793

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Alignment Scores:

Pred. No.:	7.58	Length:	48
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Percent Similarity:	41.9%	Conservative:	32
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Query Match:	3.4%	Indels:	43
DB:	3	Gaps:	7

US-10-659-800-6 (1-488) X US-09-270-767-10793 (1-485)

[illegible]

QY 83 SERASNTYRARGGLYLELEUASNTTPCY●VALVAMETLEUILLEUSERASNA1AARG 10

Db 415 -----ATTCTTAACACTTTGTGGTATATTCTGAATGAGCTCAATGCGT 37

103 LeuPheLeuGluAsnLeuIleLysTyrGlyIleLeuValAspProIleGln---ValVal 12

Db 370 TTGATAGCCTTAATTGGTATATTTTCGGCTTTAAATCTCTGAATTACGATCATGCATT 31

QY 122 SerLeuPheLeuLysAspProHisSerTrpProAlaProCysLeuValIleAlaAlaAsn 14

Db 310 AACAAATTT-----TCTGCTCGTGCTAAATTCATAATAAGCTATCAAT 26

QY 142 ValPheAlaValAlaPheGlnValGluLysArgLeuAlaValGlyAlaLeuThr--- 16

Db 265 TTATTTAGAGAGCTTAATACAGATAATATTACCTTGCTTAC-----CTTACCTTT 21

Qy 161 -----GluGlnIaGlyLeuLeuHisValAlaAsnLeuAlaThrIleLeuCys 17

Db 211 CAAATAACAACAAGGTCGTTGACTATTATTATGAAATCGTAAAGATCTATTAA 15

Qy 178 PheProAlaAlaValLeuLeuValGluSerIleThrProValGlySerLeuLeuAla 19

Db 151 CATGACATGCTGTATAAAACAATTGAADACCATAAACCTAATTGGTCAAGTCTCAAG 92

198 LeuMetAlaHisThrIleLeuPheLeuLysLeuPheSerTyrArgAspValAsnSerTrp 21

Db 91 TTAATGGCAATGTGCTGGAACCTTGAAGCGACTCTCGCTA-----GCATTCAAGTTGG 38

Qy 218 CysBArgAlaArgAlaLysAlaAlaSerAla 228

Db 37 ---CGCAGAGTAGCAGCGCGTGCTGCCGCTCA 8

RESULT 15
115 00 325 303A-6

; Sequence 6, Application US/09326203A
Patent No. 644876

; GENERAL INFORMATION:

APPLICANT: Ruezinsky, Diane
TITLE OF INVENTION: Adu1transferase Related Nucleic

TITLE OF INVENTION: Acid Sequences
PUB REFERENCE: 17045/00/WO

; CURRENT APPLICATION NUMBER: US/09/326, 203A
CURRENT FILING DATE: 1998-05-04

; PRIOR APPLICATION NUMBER: 60/088,143

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 7, 2006, 02:41:49 ; Search time 5784 Seconds
(without alignments)
5921.187 Million cell updates/sec

Title: US-10-659-800-6
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 2339354128 residues
Total number of hits satisfying chosen parameters: 32680418

Minimum DB seq length: 0
Maximum DB seq length: 500

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
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Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_g881:*
10: gb_g882:*
11: gb_g883:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	DB ID	Description
1	864	33.3	487	10	CZ559383 HMA103 Ba
2	854	32.9	473	3	BM739247 K-EST0008
3	844	32.5	454	1	BM743182 K-EST0016
4	842	32.5	452	1	AA430536 zw21605.r
5	830	32.0	467	2	BG078967 H3034B09
6	798	30.8	485	1	AM446985 88026 MAR
7	762	29.4	492	1	AW702139 uc98d11.x

8	744	28.7	452	1	AM988355 ug07e10.y
9	740	28.5	414	6	CB801052 AMGNNUC.S
10	738	28.5	407	7	CO260334 4132042.B
11	726.5	28.0	459	2	BF733499 RC6-AN006
12	720	27.8	407	6	CB771505 AMGNNUC.T
13	719	27.7	391	6	CB775155 AMGNNUC.T
14	713.5	27.5	494	1	AM391923 QV4-ST023
15	710	27.4	430	3	BM857224 K-EST014
16	707.5	27.3	490	3	BO353662 MR0-HT092
17	705	27.2	457	2	BR844007 MR2-HIT04
18	702	27.1	408	6	CB770458 AMGNNUC.T
19	698	26.9	410	3	BM851541 K-EST0132
20	689	26.6	456	3	BM836400 K-EST0112
21	672	25.9	462	6	CF364199 834132.MA
22	669	25.8	475	2	BE751071 202789.MA
23	666.5	25.7	481	3	BI753832 603027513
24	657	25.3	470	2	BF876883 PM4-EST015
25	656	25.3	479	1	AM446908 87745.MAR
26	655	25.3	470	2	BE647659 UI-M-BH1-
27	653	25.2	410	2	BE868673 601446095
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29	647.5	25.0	484	2	BE308754 601091826
30	646	24.9	422	3	BI340705 366059.MA
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36	628.5	24.2	406	6	CB807471 AMGNNUC.T
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41	612	23.6	378	1	AA478000 ZU34B07.T
42	605.5	23.3	399	1	AA453511 zx47f09.r
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ALIGNMENTS

RESULT 1
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LOCUS HMA103 BayGenomics Gene Trap Library pGTL1xT Mus musculus cDNA,
DEFINITION mRNA sequence.
ACCESSION CZ559383
VERSION CZ559383.1 GI:66858688
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 487)
BayGenomics.
http://baygenomics.ucsf.edu/
TITLE Unpublished (2001)
JOURNAL Contact: BayGenomics
COMMENT Bay Area Functional Genomics Cohortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/Baysearch.py?OPTION=EXACT&TYPE=
CELL.LINEXKEY=HMA103
Class: Gene Trap.
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/organism="Mus musculus"
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/note="vector: pGTLxlf"

ORIGIN

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Percent Similarity:	96.9%	Conservative:	4
Best Local Similarity:	94.4%	Mismatches:	5
Query Match:	33.3%	Indels:	0
DB:	10	Gaps:	0

US-10-659-800-6 (1-488) x CZ559383 (1-487)

OY 288 PheThrgInLeuGlnValGlyLeuIleGlnGlnTrpMetValProThrIleGlnAnsSer 307
DB 3 TTtACCCAGctTCAGtGGGctGATCCAGAGtGGATGctCCtTACTATCCAGAActCC 62
OY 308 MetLysProPhLeuLysAerMetAerPtySerAerGllleIleGlnAerLeuLeuValA 327
DB 63 ATGAAGCCctTCAGAGATGATGACTATTCACCGAGTCATTCAGCGctCTCTTAAAGctGGCG 122
OY 328 ValProAerHisLeuIleTrpLeuIlePhePheTyTrpLeuPheHisSerCysLeuAer 347
DB 123 GTCCCCAAGctATGATGctGGctTACTCTTCTTCTATGctTTTCCACTCCtGTCTCAAT 182
OY 348 AlaValAlaGlyLeuMetGlnPheGlyAerAerGlyPheTyAerAerPtyTrpAnsSer 367
DB 183 GCTGGGAGAGctTCTGcAGtTTGGAGACCGCGAGtTCTTACAGAGATGtGGAGATGCT 242
OY 368 GluSerValThrTyPheTrpGlnAerTrpAerIleProValHisLysTrpCysIleAer 387
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OY 388 HisPheTyLysProMetLeuAerGArgLysSerSerTyTrpMetAlaTrpThrGlyVal 407
DB 303 CAGTCTACAGctCTATGctTCAGACATGGCGACAGCAATGGtGGtGCCAGACAGAGTA 362
OY 408 PheLeuAlaSerAlaPhePheHisGlyTyLeuValSerValProLeuAerMetPheAer 427
DB 363 TTTTGGACTGcAGctCTTCTTCATGAGTAAGtGAGCGctCCCTGGAGATGtTCCGC 422
OY 428 LeuTrpAlaPheThrGlyMetMetAlaGlnIleProLeuAlaTrpPheValGlyAerPhe 447
DB 423 CTCTGGGcATTCAGCGcCATGATGctCAGTCCcACTGGcCTGATGtGGGCGcGATTC 482
OY 448 Phe 448
DB 483 TTC 485

RESULT 2

BM739247

LOCUS K-BST0008669 S2SNU668 Homo sapiens cDNA clone S2SNU668-9-H12 5', 473 bp mRNA linear EST 01-MAR-2002

DEFINITION

K-BST0008669 S2SNU668 Homo sapiens cDNA clone S2SNU668-9-H12 5',

ACCESSION

BM739247

VERSION BM739247.1 GI:19060576

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

1 (bases 1 to 473)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.U., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

COMMENT

Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.krdb.re.kr
Plate: 9 row: H column: 12
High quality sequence stop: 473.
Location/Qualifiers

FEATURES

source

1..473
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S2SNU668-9-H12"
/sex="M"
/issue_type="Ascites"
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/lab_host="Top10F"
/clone_lib="S2SNU668"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was decapped with tobacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
including EcoRI site by treatment of T4 RNA ligase. The
first strand cDNA was synthesized from oligo dt-selected
mRNA by priming with dt-tailed vector. The dt-tailed
vector was adjusted to have about 60nt. The cDNA vector
was circularized with E. coli DNA ligase after digestion
of EcoRI which site is also included in vector. An RNA
strand converted to a DNA strand by Okayama-Berg method.
The obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation
method."

ORIGIN

Alignment Scores:

Pred. No.:	3,146-75	Length:	473
Score:	854.00	Matches:	155
Percent Similarity:	98.1%	Conservative:	0
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Query Match:	32.9%	Indels:	1
DB:	3	Gaps:	0

US-10-659-800-6 (1-488) x BM739247 (1-473)

OY 245 AeraLeuLeuThrTyAerAerLeuTyTrpPheLeuPheAlaProThrLeuCyeTrpGly 264
DB 1 GACAACTGAGctTACCGcCATCTTACTTCTCTGGcCCcCAcCTTGTGctTACAGAG 60
OY 265 Leu-AerPheProAerSerProAerGlyLeuAerGlyAerPheLeuAerAerGlyLeuGly 284
DB 61 CTGCACTTTCcCCcCGctCTCCcCCGcCATCGcAAGGcCTTCTGcGcGcAAGcCTTGA 120
OY 284 UMetLeuPheThrGlnLeuGlnValGlyLeuIleGlnGlnTrpMetValProThrIle 304
DB 121 GATGctGTTCtTACcCCcAGctTCCAGtGGGcGTATCCAGAGtGGAGtGCCcCAcCAT 180
OY 304 eGlnAnsSerMetLysProPheLysAerMetAerTySerArgIleIleGlnAerGlyLe 324
DB 181 CcAGAACTCCAGtGAGcCTTCAGAGcATGAGcTACcAGcCATcATcAGAcCGcCTCT 240
OY 324 ULeuLeuAlaValProAerHisLeuIleTrpLeuIlePhePheTyTrpLeuPheHisSe 344
DB 241 GAGcTGGcGcGtCCcCAcTACcCTATGctGcTATGctTCTTCTTACTGcGcCTTTCAGTc 300
OY 344 tCysLeuLeuAlaValAlaGlyLeuMetGlnPheGlyAerAerGlyPheTyTrpAerTy 364
DB 301 CTGcCTGAATGcCGcGGcGTAGcTATcAGATTTGAGAGcCGcGAGtTCTTACcCGcAGcTG 360
OY 364 rTrpAnsSerGluSerValThrTyTrpThrGlnAerTrpAerIleProValHisLysTy 384
DB 361 GTGAACTCCAGtCTGcCATcTCTTCTGGcAGAGcTGGAGcATcCTCTGcGcAAGtG 420

Qy 384 PCGATGATGAGCTTCTACAGCCCACTGCTGACGCGGACAGCAAGTGG 472
 Db 421 GTCATCAGACCTTCTACAGCCCACTGCTGACGCGGACAGCAAGTGG 472

RESULT 3
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 DEFINITION K-EST0016267 S4SNUI Homo sapiens cDNA clone S4SNUI-6-D08 5', mRNA sequence.

ACCESSION BM743182
 VERSION BM743182.1 GI:19064511

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 454)
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52, Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.krrib.re.kr
 Plate: 6 row: D column: 08
 High quality sequence stop: 454.

FEATURES

LOCATION/Qualifiers
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 /clone_lib="S4SNUI"
 /note="Organ: Stomach; Vector: pTZ189P1; Site_1: EcoRI; Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tabacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores:
 Pred. No.: 2.98e-74 Length: 454
 Score: 844.00 Matches: 150
 Percent Similarity: 100.0% Conservatave: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 32.5% Indels: 0
 DB: 3 Gaps: 0

US-10-659-800-6 (1-488) x BM743182 (1-454)

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 Db 3 AAGAGCATGAGTACTATCAGCATCATCGAGCCCTCTGAACCTGGCGGTCCCATCAC 62

Qy 332 LeuIleTPLeuIleAphhePheTyrTrpLeuPheHisSerCysLeuAsnAlaValAlaGlu 351
 Db 63 CTCATCTGCTCATCTCTTCTTCTACCTGCTCTTCCACTCTGCTGATCCCTGCTGAG 122

Qy 352 LeuMetGlnPheGlyAspArgGluPheTyrTrpAspTrpTrpAsnSerGluSerValThr 371
 Db 123 CTCATGAGTGTGGAGACCGGAGGTCTACCGGAGTGTGGAACTCGAGTCTGTGACC 182

Qy 372 TyrPheTrpGlnAsnTrpAsnIleProValHisLysTrpCysIleArgHisPheTyrLys 391
 Db 183 TACTCTTGCGCAATGGAACATCCCTGTGCAAGTGTGATGACACACTTCTACAG 242

Qy 392 ProMetLeuArgArgGlySerSerLysTrpMetAlaArgThrGlyValPheLeuLaser 411
 Db 243 CCCATGCTTCGACGCGGCGACGACAGAGTGGACAGGAGGAGGAGTCTGCGCTCG 302

Qy 412 AlaPhePheHisGluTyrLeuValSerValProLeuArgMetPheArgLeuTrpAlaPhe 431
 Db 303 GCTTCTTCCACGAGTACCTGTGTGCGCTCTGCGAATGTTCCGCTCTGGGCGTTC 362

Qy 432 ThrGlyMetMetAlaGlnIleProLeuAlaTrpPheValGlyArgPhePheGlnGlyAsn 451
 Db 363 ACGGCACATGATGGCTCCATCCACTGGCTGTGTTGTTGGCGGCTTTTTCAGGGCAAC 422

Qy 452 TyrGlyAsnAlaAlaValAlaTrpLeuSerLeu 461
 Db 423 TATGGCAACGCGAGCTGTGTGCTGTGCTC 452

RESULT 4
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 LOCUS zw21a05.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
 IMAGE:769904 5' similar to TR:G1066810 ACYL-COENZYME A:
 CHOLESTEROL ACYLTRANSFERASE. ;, mRNA sequence.

ACCESSION AA430536
 VERSION AA430536.1 GI:2111170

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 452)
 Hillier, L., Allen, M., Bowles, J., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Scheinberg, K., Stepien, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
 WashU-NCI human EST Project
 Unpublished (1997)
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through LML ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert length: 1033 Std Error: 0.00
 Seq primer: -28m13 rev7 ET from Amerham.

FEATURES

LOCATION/Qualifiers
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 /sex="Female"
 /tissue_type="Ovarian tumor"
 /lab_host="DH10B (ampicillin resistant)"

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Db 242 TGGAAATATCCCGTGCACAGATGTGATCAGACACTTCTACAGGCTATGCTCAACACT 301
Qy 397 GYSerSerIyTPrMeCaIaArgThrgIyVaIPhleuIaIaSerIaIaPhePheIaIaG 416
Db 302 GGCAGAGCAATGGGTGGCCAGGAGATTTTTCAGCCCTCTTCCATGAG 361
Qy 417 TTTleuVaISeRyAlProIeuaRgMeTPhEaRgLeuTTPAlaPheThrgIyMeTMeIaIa 436
Db 362 TACCTAGTACGAGTTCCTCCCTGGGATGTTCCGCTCTGGGCATTTCACAGCCATGATGGCT 421
Qy 437 GHIleProIeuaIaTPrPheVaIaIyAgPhePheGInIyAaSn 451
Db 422 CAGGTCCACTGACCTGAGATTGGGCCGCAATTTCTTCAAGGAGAC 466
RESULT 6
AW446985 485 bp mRNA linear EST 25-APR-2001
LOCUS 88026 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW446985
VERSION AW446985.1 GI:6988772
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecota; Bovidae; Bovinae; Bos.
REFERENCE Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Auer,J.E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A.,
Chitko-McKown,C.G., Percec,G., Holt,I., Karanycheva,S., Liang,F.,
Quackenbush,J. and Keel,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 54 row: B column: 13
Seq primer: ATTAGGTGACACTATGAG.
FEATURES
source 1..485
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_1lb="MARC 1BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

ORIGIN
Alignment Scores:
Pred. No.: 1,38e-69 length: 485
Score: 798.00 Matches: 149
Percent Similarity: 85.5% Conservative: 4
Best Local Similarity: 83.2% Mismatches: 8
Query Match: 30.8% Indels: 18

DB: 1 Gaps: 2
US-10-659-800-6 (1-488) x AW446985 (1-485)
Qy 202 ThrIIeIePheIeUeIyIeUePheSeRyYrARgAsPvaIaIaSeRyTPrCySaRgArGaIa 221
Db 3 ACCATCTCTCTCTCAAGCTGTCTCTCAACGGGAGCTCAACCTCGTGCCAGAGCGC 62
Qy 222 ArgAlaIyAlaIaIaSerIaIaGlyIyIyVaIaIaSeRyAlaIaIaIaProIaIaIa 241
Db 63 AGS-----GCTGGGCCAAGGCCAAGGCTGCTTGGCA-----95
Qy 242 SeRyYrProAsPAsIeUeThryYrARgAsPLeuYrYrPheUePheAlaProThrIeU 261
Db 96 -----GATCTCTACTTCTCTCTCTTGGCCCCACCG 128
Qy 262 CyRyTgIyIeUaIaIaPheProIaRgSeRProARgIleARgIyARgPheIeUeUaRgAg 281
Db 129 TGTCAAGAGCTCAACTCCCGGCTCCCGGCTCCCGGCTCCGAAAGCGCTTCTGCGCGGCA 188
Qy 282 ITeIeUgIuMeTleUePhePheThrgIeUeGInIyIeUeIeGInIeThrMeTvaI 301
Db 189 CTCTGAGATCTGTCTCTCAACCGCTCCAGGTGGGCTAATCCAGAGTGAATGTC 248
Qy 302 ProThrIIeGInIaIaSeRMeTlySProPheIyAsPMeTAsPtyrSeRArgIleIeGIn 321
Db 249 CCGGCATTCAGAACTCCATGAAAGCCCTTCAAGACATGATACCTCCGCAATCGAGAG 308
Qy 322 ArgIeUeIyIeUaIaIaIaProIaIaIaIeUeIeTPrIeUeIePhePheYrYrIeU 341
Db 309 CCGCTCTCAAGCTGCGGCTCCCAACCACTCATCTGCTCATCTTCTTACTGCGCTC 368
Qy 342 PheHISerCyIeUaIa 361
Db 369 TTTCACTCTGTGCTGAAGCCGCTGCTGCTCATGACATTTGGAGACCGCAGATTCTAC 428
Qy 362 ArgAsPTrPTrAsIeRyIeUeIa 380
Db 429 CCGGACTGTGAATCTCGAATCATCACTTCTTGGCAGAACTCGAATCTCCT 485
RESULT 7
AW702139 492 bp mRNA linear EST 18-APR-2000
LOCUS u998d11.x1 NCI CGAP Mam10 Mus musculus cDNA clone IMAGE:2939157 3'
DEFINITION similar to TR:Q92ZA7 Q92ZA7 DIACYLGIVCEROL ACYLTRANSFERASE. ;, mRNA
sequence.
ACCESSION AW702139
VERSION AW702139.1 GI:7586288
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
1 (bases 1 to 492)
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: Lohar Henniphausen Ph.D., Jeffrey Green M.D.,
Gilbert Smith, Ph.D., William Muller, M.D.,
cDNA Library Preparation: M. Benito Soares, Ph.D., M. Fatima
Bonafide, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
image.llnl.gov/image/html/resources.shtml
MGI:1051577
Possible reversed clone: similarity on wrong strand

Seq primer: -40UP from Glibco
High quality sequence stop: 448.
Location/Qualifiers

FEATURES

SOURCE

1..492
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:293157"
/cissue_type="pooled mammary gland tumors"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NCI_CGAP_Mam10"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled mammary gland tumors with a Not I - oligo(dT) primer (5' TGTTACCAATCTGAAGTGGAGCCGCCACTAGTTTATTTTATTTT 3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bernaldo."

ORIGIN

Alignment Scores:

Pred. No.: 5,898-66 Length: 492
Score: 762.00 Matches: 131
Percent Similarity: 97.2% Conservative: 8
Best Local Similarity: 91.6% Mismatches: 4
Query Match: 29.4% Indels: 0
DB: 1 Gaps: 0

US-10-659-800-6 (1-488) x AM702139 (1-492)

QY 342 PheHISserCYeLeuAaAlaValAlaGluLeuMetGlnPheGlyAspArgGluPheTyr 361
DB 6 TTCCACTCTCTGCTCAATGCTGTGGCAGAGCTTGTGAGAGCCGAGTTCTAC 65

QY 362 ArgAspTPPTTPAsnSerGluSerValThrTyrPheThrGlnAsnTrpAsnIleProVal 381
DB 66 AGAGATTGGTGAATGCTGAGTCTGACCTTCTTGGCAGAACTGGAAATCCCGTG 125

QY 382 HisIstYTPCYailAArgHisPheTyrIlySPrometLeuArgArgGlySerSerIlySTP 401
DB 126 CACAAGTGTGATCGACACCTTCAAGCCTATGCTAGACAGGCGCAAGCAATGG 185

QY 402 MetAlaArgThrGlyValPheLeuAlaSerAlaPhePheHisGluTyrLeuValSerVal 421
DB 186 GTGGCCAGGACGAGAGTATTTTGTACCTCAGCCTTCTCCATGAGTACCTAGAGCGTT 245

QY 422 TrpLeuArgMetPheArgLeuTrpAlaPheThrGlyMetMetAlaGlnIleProLeuAla 441
DB 246 CCCCTGGGAGTGTCCGCTCTGGGCATTCACAGCCATGATGCTCAGGTCCTCAGCTGGCC 305

QY 442 TrpPheValGlyArgPhePheGlnGlyAsnTyrGlyAsnAlaAlaValTrpLeuSerLeu 461
DB 306 TGGATTGTGGCCGATTCTTCCAGGGAATGGAATGCAAGCTGTGGTGACACATC 365

QY 462 IleIleGlyGlnProIleAlaValLeuMetTyrValHisAspTyrTyrValLeuAsnTyr 481
DB 366 ATCATTTGGGCAACCGGTGCTGTGCTCATGTATGTCCAGACTACTACGTGTCAATAC 425

QY 482 GlnIlePro 484
DB 426 GATGCCCA 434

RESULT 8
LOCUS AM988355 452 bp mRNA linear EST 02-JUN-2000
DEFINITION ugm07e10.y1 Soares_mammary_gland_NMLNG Mus musculus cDNA clone

IMAGE:1530954 5' similar to TR:Q922A7 Q922A7 DIACYLGLYCEROL
ACYLTRANSFERASE.1, mRNA sequence.
ACCESSION AM988355

VERSION AM988355.1 GI:8183481
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapdb-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:947054

Seq primer: -40NP from Glibco.
Location/Qualifiers
1..452
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1530954"
/sex="Female (lactating)"
/cissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bernaldo."

FEATURES

SOURCE

US-10-659-800-6 (1-488) x AM988355 (1-452)

ORIGIN

Alignment Scores:

Pred. No.: 3,336-64 Length: 452
Score: 744.00 Matches: 128
Percent Similarity: 97.1% Conservative: 8
Best Local Similarity: 91.4% Mismatches: 4
Query Match: 28.7% Indels: 0
DB: 1 Gaps: 0

US-10-659-800-6 (1-488) x AM988355 (1-452)

QY 345 CysLeuAaAlaValAlaGluLeuMetGlnPheGlyAspArgGluPheTyrArgAspTrp 364
DB 3 TGTCTCATGCTGTGGCAGAGCTTCTGCAAGTTTGGAGACCGCGAGTTCTACAGAGATTGG 62

QY 365 TrpAsnSerGluSerValThrTyrPheThrGlnAsnTrpAsnIleProValHisIstYTP 384
DB 63 TGGATTGTGAGTCTGACCTACTTGTGGCAAGATGGAATATCCCGTGCACAAAGTGG 122

QY 385 CysIleAArgHisPheTyrIlySPrometLeuArgArgGlySerSerIlyTrpMetAlaArg 404
DB 123 TGCATCAACACCTTCTACAACTATGCTCAGACATGGCAACAGAAATGGGTGGCCAGG 182

QY 405 ThrGlyValPheLeuAlaSerAlaPhePheHisGluTyrLeuValSerValProLeuArg 424
DB 183 ACAGAGATTTTGTACCTCAGCCTTCTCCATGATGTAAGTGAAGGTTCCCTGGCGG 242

QY 425 MetPheArgLeuTrpAlaPheThrGlyMetMetAlaGlnIleProLeuAlaTrpPheVal 444
DB 243 ATGTTCGCTCTGGGCATTCACAGCCATGATGCTCAGTCCACTGACTGGATTGGT 302

QY 445 GlyArgPhePheGlnGlyAsnTyrGlyAsnAlaAlaValTrpLeuSerLeuIleIleGly 464
DB 303 GCGCATTTCTTCCAAAGGAATATGCAATGCAATGCAAGTGTGGTGACATCATTTGGG 362

QY 465 GlnProIleAlaValLeuMetTyrValHisAspTyrTyrValLeuAsnTyrGlnIlePro 484

Db 363 CAACCGTGGCTGTGCTCATGTATGTCCAGCACTACTAGTGTCTCACTACGATGCCCA 422
RESULT 9
LOCUS CB801052 414 bp mRNA linear EST 16-MAY-2003
DEFINITION AMGNKUC:SRBP2-00118-D4-A srpb2 (10220) Rattus norvegicus cDNA clone
CB801052
ACCESSION CB801052
VERSION CB801052.1 GI:29913930
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE
AUTHORS 1 (bases 1 to 414)
TITLE Amgen EST Program.
JOURNAL Amgen Rat EST Program
COMMENT Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00118 row: d column: 4.
Location/Qualifiers
1..414
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="srpb2-00118-d4"
/tissue_type="prostate tissue"
/clone_1ib="srpb2 (10220)"
/note="Vector: pSPORT1. Site 1: SalI; Site 2: NotI; rat
prostate normalized double selected poly(A+) mRNA size
fraction > 1 Kb"
ORIGIN
Alignment Scores:
Pred. No.: 7 376-64 Length: 414
Score: 740.00 Matches: 129
Percent Similarity: 98.5% Conservative: 6
Best Local Similarity: 94.2% Mismatches: 2
Query Match: 28.5% Indels: 0
Gaps: 0
US-10-659-800-6 (1-488) x CB801052 (1-414)
QY 303 Thrllglnasnsermetlyspophelyaspmetyrserargllellegluarg 322
DB 3 ACTATCCAGAACTCCATGAAAGCCCTTCAAGAGCATGAGATTATTCAGATCATTTAGCGCT 62
QY 323 LeuLeuLYbLeuAlaValaProbanHlbleuiletrpleuilephepheyrrtpleuphe 342
DB 63 CTCTTAAAGCTGGCGCTCCCAACCATCGATATGCGTCATCTTCTTATTTGGCTTTTC 122
QY 343 HlsserCybleuasnAlaValaAlaGluLeuMetGlnpheGlyAspArgGluubheYrarg 362
DB 123 CACTATGCTCTAAAGCTGTGGCAGAGCTCGCAGTTGGAGACCGCAGATTCTACAG 182
QY 363 AspTPTPAsnserGluSerValThrtYrPheTrGlnasnTrpAnlleProValHis 382
DB 183 GACTGTGGAAATCGCAGCTGTCTACCTTCTTTGGCAGAACTGGAAATCCCCGGCGAC 242
QY 383 LybTTPCybleargHllepheyrrlyspPomMetLeuArgGlySerSerlystrpMet 402
DB 243 AAGGTGTGATCAGACACTTCTTACAAAGCCTATGCTCAGACTGGGCGAGCAAAATGAGATG 302
QY 403 AlaargTrnGlyValaPheLeuAlaSerAlaPhePheHlAgLuTrpleuValaSerValPro 422
DB 303 GCCAGACTGGGGCTCTTTTGGCGTCAAGCTTCTTCCATAGACTACTAGACATTTCCC 362
QY 423 LeuArgMet PheArgLeuTrpAlaPheTrnGlyMetMetAlaGlnlePro 439

Db 363 CTGAGGATGTTCGGCTCTGGGCATTACAGCCATGATGCTCAGGTCCCA 413
RESULT 10
LOCUS CO260334 407 bp mRNA linear EST 23-JUN-2004
DEFINITION 4132042 BARC 8BOV Bos taurus cDNA clone 8BOV_57F07 5', mRNA
sequence.
ACCESSION CO260334
VERSION CO260334.1 GI:49145172
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE
AUTHORS 1 (bases 1 to 407)
TITLE Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and
Matukumalli,L.K.
JOURNAL Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
COMMENT Unpublished (2004)
Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI
BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '- -trim_fast. Vector identified
by cross match using options -mismatch 12 -mnscore 18
Plate: 57 row: F column: 07
Seq primer: CCTATTAGTGCACACTATAGAAC
High quality sequence stop: 407.
Location/Qualifiers
1..407
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="8BOV_57F07"
/sex="Female"
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="PHIOB Tona"
/clone_1ib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
NotI; Site 2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 lactating, proximal duodenum,
jejunum, distal ileum, colon, 1/5 Neonatal, proximal
duodenum, jejunum, distal ileum"
ORIGIN
Alignment Scores:
Pred. No.: 1 146-63 Length: 407
Score: 738.00 Matches: 128
Percent Similarity: 97.8% Conservative: 3
Best Local Similarity: 95.5% Mismatches: 3
Query Match: 28.5% Indels: 0
Gaps: 0
US-10-659-800-6 (1-488) x CO260334 (1-407)
QY 309 LysPProphelyaspmetyrserargllellegluargLeuLYbLeuAlaVal 328
DB 2 AAGCCCTTCAAGAGCATGAGCTATTCGCCGACATCGAGGCGCTCTGAGAGCTGGCGGCT 61
QY 329 ProbanHlbleuiletrpleuilephepheyrrtpleupheHlsserCybleuasnAla 348
DB 62 CCCAACCACTCATGTGCTCATCTTCTTCTACTGGCTCTTCCACCCCTGCGCTGAGACGCC 121

QY 349 ValAlaGluLeuMetGlnPheGlyAspArgGluPheTyrArgAspTrpTrpAsnSerGlu 368
 Db 122 GTGGCTGAGCTCATCTCAGTTGGAGACCGCGAGTTCTACCGGAGCTGGGAACTCCGAG 181
 QY 369 SerValThrTyrPheTrpGlnAsnTrpAsnIleProValIleGlyTrpCysIleArgHis 388
 Db 182 TCATCACCCTACTTCTGGCAGAACCTGGAACATCCCTGTTCCAGAGTGGCATCAGAC 241
 QY 389 PheTyrIleProMetLeuArgArgGlySerSerIleTyrMetAlaArgThrGlyValPhe 408
 Db 242 TTCTCAAGACCATCTCGCGCGGCGAGCAAGTGGGCGAGCAGAGCGCAGTGT 301
 QY 409 LeuAlaSerAlaPhePheIleGlyTyrLeuValSerValProLeuArgMetPheArgLeu 428
 Db 302 CTGGCTCCCGCTCTTCTCCACGAGTACTGTGGAGAGTCCCTCTGGCGCATGTTCCGCTC 361
 QY 429 TrpAlaPheThrGlyMetMetAlaGlnIleProLeuAlaTrp 442
 Db 362 TGGGCTTCACTCCGCGATGATGGCGCAGATCCCGCTGGCTGG 403
 RESULT 11
 LOCUS BF733499/c 459 bp mRNA linear EST 09-JAN-2001
 DEFINITION RC6-AN0063-081000-011-B03 AN0063 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF733499
 VERSION BF733499.1 GI:12058735
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 459)
 Diara Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
 Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
 Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
 Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V.,
 O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
 Simpson, A. J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800
 TITLE Contact: Simpson A.J.G.
 JOURNAL Laboratory of Cancer Genetics
 PUBMED Institute for Cancer Research
 COMMENT Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel.: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FADESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC6&c2=RC6-AN0063-
 081000-011-B03&c3=2000-10-08&c4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 26
 High quality sequence stop: 458.
 Location/Qualifiers
 1..459
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="AN0063"
 /note="Organ: amnion normal; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN
 Alignment Scores:
 Pred. No.: 1,96e-62 Length: 459
 Score: 726.50 Matches: 147
 Percent Similarity: 98.7% Conservative: 1
 Best Local Similarity: 98.0% Mismatches: 1
 Query Match: 28.0% Indels: 1
 DB: 2 Gaps: 1
 US-10-659-800-6 (1-488) x BF733499 (1-459)
 QY 103 LeuPheLeuGluAsnLeuIleGlyTyrGlyIleLeuValaAspProIleGlnValaSer 122
 Db 457 TTATTTCGAGAACCTCATCAGATAGCATCTCGGTGGAGACCCATCCAGTGGTTCT 398
 QY 123 LeuPheLeuValaAspProHisSerTrpProAlaProCysLeuValIleAlaAlaAsnVal 142
 Db 397 CTGTTCTGAAGAGATCTCTATAGCTGGCCGCCCATGCTGTATTGCGGCCAATGTC 338
 QY 143 PheAlaValAlaAlaPheGlnValGluValaArgLeuAlaValaGlyAlaLeuThrGluGln 162
 Db 337 TTGCTGTGGCTGATTCACAGTTGAGAACCGCTGGCGGTGGTCCCTGACGAGCAG 278
 QY 163 AlaGlyLeuLeuLeuHisValaAlaAsnLeuAlaThrIleLeuCysPheProAlaAlaVal 182
 Db 277 GCGGGA---CTGCTGCACGTGGCCCACTGGCCACCATTTGTGTTTCCAGCGGCTGTG 221
 QY 183 ValLeuLeuValaGluSerIleThrProValaGlySerLeuLeuAlaLeuMetAlaHisThr 202
 Db 220 GTCTTACGTGGTGAATCATGCTTCAGTGGGCTCCCTGCGGCTGATGGCGCACACC 161
 QY 203 IleLeuPheLeuValaLeuPheSerTyrArgAspValaAsnSerTrpCysArgArgAlaArg 222
 Db 160 ATCTCTTCTTCAAGCTTTCTCTCAACCGCAGCAGCATCATGTTGCCGAGGCGCAGG 101
 QY 223 AlaValaAlaAlaSerAlaGlyValaValaAsnSerAlaAlaAlaProHisThrValSer 242
 Db 100 GCCAAGGCTGCTCTGACGAGGAAGAGCCAGCATGCTGTGCCGCCACACCGTGAGC 41
 QY 243 TyrProAspAsnLeuThrTyrArgAspLeu 252
 Db 40 TACCCGACAACTACCTACCGCATCTA 11
 RESULT 12
 LOCUS CB771505 407 bp mRNA linear EST 16-MAY-2003
 DEFINITION AMGNND:TXXP1-00014-D10-A txp1 (10556) Rattus norvegicus cDNA
 clone txp1-00014-d10 5', mRNA sequence.
 ACCESSION CB771505
 VERSION CB771505.1 GI:29859896
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Rattus.
 1 (bases 1 to 407)
 Amgen EST Program.
 Amgen Rat EST Program
 Unpublished (2003)
 COMMENT Contact: Dan Fitzpatrick
 Amgen, Inc
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00014 row: d column: 10.
 Location/Qualifiers
 1..407
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="txp1-00014-d10"
 /tissue_type="prostate"

FEATURES

FEATURES

ORIGIN /clone_lib="txrpl (10556)"
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rat prostate"

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Best Local Similarity: 95.6% Mismatches: 1
Query Match: 27.8% Indels: 1
DB: 6 Gaps: 0

US-10-659-800-6 (1-488) x CB771505 (1-407)

QY 265 LeuAnpPheProARXSeProARgllLeARgLYsARgPheLeuLeuARgllLeuGlu 284
DB 1 CTCACCTTCCCTCGATCCCGCAATACGAAAGCCCTTCTCTACGGCGGCTTCTTGAG 60
QY 285 MetLeuPhePheThrGlnLeuGlnValGlyLeuIleGlnGlnTrpMetValProThrIle 304
DB 61 ATGCTCTTTTTCACCCAGCTTCAAGTGGGCTGATCCAGCATGATGATGCTCTACTAT 120
QY 304 eGlnAnSerMetLYsProPheLYsAPMeLAPTYrSerArgIleIleGlnArgLeuLeu 324
DB 121 CCAAGACTCCATGAGACCCCTTCAAGAGACATGAGACTATTCACGATCATGAGCGTCTT 180
QY 324 uLYsLeuAlaValProAnHISLeuIleTrpLeuIlePhePheTYrTrpLeuPheHIS 344
DB 181 AAGCTGGCGGCTCCCAACCATGTGATGGCTCATCTTCTTATGGCTTTTCCACATC 240
QY 344 CYsLeuAnAlaValAlaGluLeuMeGlnPheGlyAsPARgLYsARgLYsARgAsPTR 364
DB 241 ATGCTCATGCTGTGGCAGAGCTCTGAGATTGAGACCCGAGTTCTACAGGAGCTG 300
QY 364 TrpAnSerGluSerValThrTYrPheTrpGlnAnTrpAnIleProValHISLYSTR 384
DB 301 GTGGAATGCTGAGTCTGTACCTACTTTTGGCAGAACTGGAATATCCCGTGCACAAATG 360
QY 384 CYsIleArgHISpHeTYrLYsProMeLeuArgGlySerSer 399
DB 361 GTGCATCAGACACTTCTACAAAGCTATGCTCAGACTGGGACGACAAAC 406

RESULT 13
CB775155 391 bp mRNA linear EST 16-MAY-2003
LOCUS AMGNND:TRXP1-00005-C5-A txrpl (10556) Rattus norvegicus cDNA clone
DEFINITION txrpl-00005-C5 5', mRNA sequence.
ACCESSION CB775155
VERSION CB775155.1 GI:29863546
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 391)
AUTHORS Angen EST Program.
TITLE Angen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00005 row: c column: 5.
Location/Qualifiers

FEATURES
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/organism="Rattus norvegicus"
/mol_type="mRNA"
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ORIGIN /note="Vector: pYVA-41L; Site_1: HindIII; Site_2: NotI;
rat prostate"

Alignment Scores:
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Score: 719.00 Matches: 127
Percent Similarity: 100.0% Conservative: 3
Best Local Similarity: 97.7% Mismatches: 0
Query Match: 27.7% Indels: 0
DB: 6 Gaps: 0

US-10-659-800-6 (1-488) x CB775155 (1-391)

QY 265 LeuAnpPheProARXSeProARgllLeARgLYsARgPheLeuLeuARgllLeuGlu 284
DB 1 CTCACCTTCCCTCGATCCCGCAATACGAAAGCCCTTCTCTACGGCGGCTTCTTGAG 60
QY 285 MetLeuPhePheThrGlnLeuGlnValGlyLeuIleGlnGlnTrpMetValProThrIle 304
DB 61 ATGCTCTTTTTCACCCAGCTTCAAGTGGGCTGATCCAGCATGATGATGCTCTACTATC 120
QY 305 GlnAnSerMetLYsProPheLYsAPMeLAPTYrSerArgIleIleGlnArgLeuLeu 324
DB 121 CAGAACTCCATGAGACCCCTTCAAGAGACATGAGACTATTCACGATCATGAGCGTCTT 180
QY 325 LYsLeuAlaValProAnHISLeuIleTrpLeuIlePhePheTYrTrpLeuPheHIS 344
DB 181 AAGCTGGCGGCTCCCAACCATGTGATGGCTCATCTTCTTATGGCTTTTCCACTCA 240
QY 345 CYsLeuAnAlaValAlaGluLeuMeGlnPheGlyAsPARgLYsARgLYsARgAsPTR 364
DB 241 ATGCTCATGCTGTGGCAGAGCTCTGAGATTGAGACCCGAGTTCTACAGGAGCTG 300
QY 365 TrpAnSerGluSerValThrTYrPheTrpGlnAnTrpAnIleProValHISLYSTR 384
DB 301 TGGGAATGCTGAGTCTGTACCTACTTTTGGCAGAACTGGAATATCCCGTGCACAAATG 360
QY 385 CYsIleArgHISpHeTYrLYsProMeLeu 394
DB 361 TGCAATCAGACACTTCTACAAAGCTATGCTC 390

RESULT 14
AW391923 494 bp mRNA linear EST 04-FEB-2000
LOCUS AW391923
DEFINITION QV4-ST0233-251199-041-907 ST0233 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW391923
VERSION AW391923.1 GI:6896582
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 494)
AUTHORS HCCP <http://www.ludwig.org.br/ORGSTES>.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV4&t2=QV4-ST0233-251199-041-907&t3=1999-11-25&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 494.
Location/Qualifiers

FEATURES


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Db      243 GTGGGTGCCCTGACGAGCAGCGGGGACTGCTGCACTGCGCCACCTGGCCACCAATT 302
OY      176 LeuCySPheProAlaIaValValLeuLeuValGluSerIleThrProValGlySerLeu 195
Db      303 CTGTGTTTCCACGCGGCTGTGCTTACTGTTGAGTCTATCACTCCAGTGGGCTCTCCCTG 362
OY      196 LeuAlaLeuMetAlaHisThrIleLeuPheLeuTyrLeuPheSerTyrArgAspValAsn 215
Db      363 CTGGCGCTGATGGCGCACACATCCTCTTCTCAAGCTCTTCTCTACCGCGAGCTCAAC 422
OY      216 SerTTP 217
Db      423 TCATGG 428
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Search completed: May 7, 2006, 04:18:29
Job time : 5792 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: May 6, 2006, 19:36:32 ; Search time 1363 Seconds
(without alignments)
3579.277 Million cell updates/sec

Title: US-10-659-800-6
Perfect score: 2594
Sequence: 1 MGDGSSRRRTGSRPSHG.....VLMVHYDVVINYEAPAAEA 488

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 7170814

Minimum DB seq length: 0
Maximum DB seq length: 500

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blowum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	842	32.5	452	6	ABL81686 Human ova
2	644	24.8	450	6	AAD40443 Bovine di
3	612	23.6	371	6	ABL82916 Human ova
4	603.5	23.3	433	4	AAS41185 CDNA enco

5	603.5	23.3	433	4	ABA06648 Human CDN
6	603.5	23.3	433	6	ABV83985 Human pol
7	567	21.9	447	9	ACH42044 Human foe
8	332	12.8	471	9	ACH14767 Human adu
9	330.5	12.7	380	6	AB085322 Arabidops
10	232	8.9	299	3	AAD45382 DNA enco
11	232	8.9	299	3	AAB88845 Mouse acy
12	222.5	8.6	400	13	ADU81175 Ryegrass
13	217	8.4	420	12	ACH92522 Human gen
14	199	7.7	400	6	AAD04442 Bovine di
15	197.5	7.6	381	3	AAD45387 Acyl-CoA:
16	197.5	7.6	381	3	AAB88836 C. elegan
17	191.5	7.4	393	9	ACH46527 Human inf
18	191.5	7.4	399	9	ACH46069 Human inf
19	191.5	7.4	401	9	ACH45947 Human inf
20	191.5	7.4	418	9	ACH45946 Human inf
21	188.5	7.3	401	9	ACH46143 Human inf
22	187.5	7.2	401	9	ACH46631 Human inf
23	181	7.0	470	6	ABL93444 Arabidops
24	177.5	6.8	365	9	ACH47212 Human inf
25	173.5	6.7	402	9	ACH46232 Human inf
26	171.5	6.6	378	13	ADDS4498 Bacterial
27	170	6.6	275	3	AAD45374 Acyl-CoA:
28	170	6.6	275	3	AAB88840 Soybean a
29	170	6.6	275	5	AAS01313 Soybean s
30	164.5	6.3	383	9	ACH47844 Human inf
31	164	6.3	225	3	AAA10204 Rat liver
32	159	6.1	421	6	ABK29584 Colon ade
33	155	6.0	253	3	AAD45376 Acyl-CoA:
34	155	6.0	253	3	AAB88849 Maize acy
35	155	6.0	253	5	AAS01315 Maize etc
36	148	5.7	357	12	ADDS05089 Gene #186
37	143.5	5.5	386	13	ADU14134 Solid tum
38	140.5	5.4	258	13	ADU81173 Ryegrass
39	130.5	5.0	408	9	ACH46887 Human inf
40	127	4.9	267	3	AAD45373 Acyl-CoA:
41	127	4.9	267	3	AAB88841 Soybean a
42	127	4.9	267	5	AAS01312 Soybean s
43	123.5	4.8	234	3	AAD45372 Acyl-CoA:
44	123.5	4.8	234	3	AAB88839 Soybean a
45	123.5	4.8	234	5	AAS01311 Soybean s

ALIGNMENTS

RESULT 1
ABL81686
ID ABL81686 standard; CDNA; 452 BP.
XX
AC ABL81686;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human ovarian cancer related CDNA clone SEQ ID NO:4664.
XX
KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200192581-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US017756.
XX
PR 26-MAY-2000; 2000US-0207484P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Aigate PA, Harlocker SL, Jones R;
XX
DR WPI; 2002-122075/16.
XX

CC basis of DGAT1 action and to test a substance for the ability to prevent,
CC slow or enhance DGAT1 activity. The present sequence is bovine DGAT1 cDNA
CC fragment used to illustrate the method of the invention
XX
SQ Sequence 450 BP; 77 A; 165 C; 117 G; 91 T; 0 U; 0 Other;

SQ Sequence 450 BP; 77 A; 165 C; 117 G; 91 T; 0 U; 0 Other;

Alignment Scores:

Pred. NO.:	8.87e-52	Length:	450
Score:	644.0	Matches:	126
Percent Similarity:	89.3%	Conservative:	7
Best Local Similarity:	84.6%	Mismatches:	12
Query Match:	24.8%	Indels:	4
DB:	6	Gaps:	1

US-10-659-800-6 (1-488) X AAD40443 (1-450)

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Oy 182 aValleuLeuValGluSerIleThrProValGlySerLeuLeuAlaLeuMetAlaHis 200
Db 3 GGAGCGCTTCTCTCCAGTCTATCACTCCAGTGGAGCTCCGCTGGCCGTGATGTTAC 62
Oy 202 ThrIleLeuPheLeuIleuPheSerTyrArgAspValAsnSerTyrCysArgArg-- 220
Db 63 ACCATCTCTTCTCTCAAGCTGTTCTCTACCGGAGATGTAACCTTGATGCCAGAGGCC 122
Oy 221 -----AlaArgAlaIysAlaIaIaSerAlaGlyIleValAlaSerAlaIaIa 237
Db 123 AGGGCTGGGGCCAGAGGCCAAGGCTGTTGGCGAGTAAGAGGCCAACGGGGAGCTGCC 182
Oy 238 ProHisThrValSerTyrProAspAsnLeuThrTyrArgAspLeuTyrTyrPheLeuPhe 257
Db 183 CAGCCGACCGTAGACGTACCCCGAACCACTGACTACCGGATCTCTACACTCTTCTTC 242
Oy 258 AlaProThrLeuCysTyrGluLeuAsnPheProArgSerProArgIleArgIleArgPhe 277
Db 243 GCCCCACCCCTGTGCACAGGCTCACTTCCCCGCTCCCCCGCATCCCAAGGCCCTTC 302
Oy 278 LeuLeuArgArgIleLeuGluMetLeuPhePheThrGluLeuGluValGlyLeuIleGln 297
Db 303 CTGCTGGCGGCACTCTCGAGATGCTGTTCTCACCCAGCTCCAGGTGGGGCTGATTCAG 352
Oy 328 GlnTrpMetValProThrIleGlnAsnSerMetIysProPheIleAspMetAspTyrSer 317
Db 363 CAGTGGATGATCCCGGCGATCCAGAACTCAATGAAGCCCTTCAAAGACATGACTACTCC 422
Oy 318 ArgIleIleGluArgLeuLeuIleLeu 326
Db 423 CGCATCTGGAGCGGCTCTGAAGCTG 449

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RESULT 3

ID ABL82916 standard; cDNA; 371 BP.

AC ABL82916;

DT 17-MAY-2002 (first entry)

DE Human ovarian cancer related cDNA clone SEQ ID NO:5894.

KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

Homo sapiens.

PN W0200192581-A2.

PD 06-DEC-2001,

PF 29-MAY-2001; 2001WO-US017756.

PR 26-MAY-2000; 2000US-0207484P.

PA (CORI-) CORIXA CORP.

PI Algate PA, Harlocker SL, Jones R;

XX WPI; 2002-122075/16
DR

PT Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide.

PS Claim 1; SEQ ID NO 5894; 489pp; English.

The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of an ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient. Where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting and expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known techniques

50 Sequence 371 BP; 65 A; 136 C; 89 G; 81 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7,48e-49	Length:	37
Score:	612.00	Matches:	122
Percent Similarity:	99.2%	Conservative:	0
Best Local Similarity:	99.2%	Mismatches:	1
Query Match:	23.6%	Indels:	1
DB:	6	Gaps:	0

US-10-659-800-6 (1-488) X ABL82916 (1-371)

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Db	1	GTTGAGTATACCTCCAGTGGGCTCCCTGGCGGCTATGGC - CACCACATCTCTTC	59
QY	206	LeuIysLeuPheSerTyrArgAspValAsnSerTPCyAspArgAlaArgAlaIysAla	225
Db	60	CTCAAGCTCTTCTCTACCGGACGCTCAACTCATGTGTGGCAGGGCCAGGGCAAGCT	119
QY	226	AlaSerAlaGlyLysLysAlaAspSerSerAlaAlaAlaProHisThrValSerTyrProAsp	245
Db	120	GCTCTGCAGGGAGAAAGGCCAGCAGTCTGCTGCCGCCACACCCGTAGCTACCCGGAC	179
QY	246	AsnLeuThrTyrArgAspLeuTyrTyrPheLeuPheAlaProThrIleuGlyTyrGluLeu	265
Db	180	AATCGACTTACCGGGATCTCTACTACTTCTCTTGCCGCCACCTGTGTACGAGCTC	239
QY	266	AsnPheProArgSerProArgIleArgLysBatPheLeuLeuArgArgIleLeuGluMet	285
Db	240	AACCTTCCCGCTCTCCCGCATCCGGAAGCGCTTCTGTCTGAGCAGATCTTGAGATG	299
QY	286	LeuPhePheThrGlnLeuGlnValGlyLeuIleGlnGlnTTPMetValProThrIleGln	305
Db	300	CTGTCTCTTACCCACAGCTCCAGGTGGGGCTGATCCAGCAGTGAATGATCCCCACATCCAG	359
QY	306	AsnSerMetLys	309
Db	360	AATCTCATGAAG	371

RESULT 4

AAS41185

ID AAS41185 standard; cDNA; 433 BP.
XX AAS41185;
AC
XX 17-DEC-2001 (first entry)
DT
XX
DE cDNA encoding novel human enzyme polypeptide #401.
XX
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW lysase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotropic; anticoagulant; ss.
XX
OS Homo sapiens.
XX
PN W0200155301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001239.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
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PR 05-SEP-2000; 2000US-0229509P.
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PR 06-SEP-2000; 2000US-0230437P.
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PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
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PR 01-NOV-2000; 2000US-0244617P.
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PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246529P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249255P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249298P.
PR 17-NOV-2000; 2000US-0249300P.

PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0228287P.
PR 01-SEP-2000; 2000US-0228343P.
PR 01-SEP-2000; 2000US-0228344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0231415P.
PR 08-SEP-2000; 2000US-0232080P.
PR 12-SEP-2000; 2000US-0232081P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234979P.
PR 25-SEP-2000; 2000US-0234984P.
PR 26-SEP-2000; 2000US-0234984P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 01-NOV-2000; 2000US-0244674P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251865P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PA (HUMA) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-476161/51.
DR P-PSDB; ABB10426.
XX
XX Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PI condition.
XX
XX
XX Claim 1; SEQ ID NO 314; 859pp + Sequence Listing; English.
PS
XX The present invention provides human cDNAs, proteins and related genomic
CC DNA. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a cDNA of the invention
XX
SQ Sequence 433 BP; 87 A; 128 C; 111 G; 103 T; 0 U; 4 Other;
Alignment Scores:
Pred. No.: 6,04e-48 Length: 433
Score: 603.50 Matches: 126
Percent Similarity: 87.2% Conserves: 3
Best Local Similarity: 85.1% Mismatches: 12
Query Match: 23.3% Indels: 7
DB: 4 Gaps: 1
US-10-659-800-6 (1-488) x ABA06648 (1-433)
Qy 264 GluLeuAenPhProArSerProArgIlaRgLySaRPhLeuLeuArgArgIleu 283
Db 1 GAGCTCAACTTCCCGCTCCCGATCCGGAAGCCCTTCTGCTCGACGATCCTT 60
Qy 284 GluMetLeuPhPheRthGlnLeuGlnValGlyLeuIleGlnIntPMeValProThr 303
Db 61 GAGATGCTGTTCTTCAACCACTCCAGGTGGGCTGATCCAGAGTGATGTCCTCCACC 120
Qy 304 IleGlnAnSerMetLySProPhelyAspMetAspTyrsArgYlleIleGluArgLeu 323
Db 121 ATCCAGAACTCATTCAAGAGCCCTTCAAGGACATGACTACGATCATCATGAGCGCTC 180

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Qy 324 LeuLysLeuAlaValProAsnHisLeuIleTyrPheLeuIlePhePheTyrTrpPhePheHis 343
Db 181 CTGAAGCGGGGGGCTCCCAATCACTCATCTGGCTCATCTTCTTACTGGCTCTTCCAC 240
Qy 344 SerCysLeuAaAlaValAlaGluLeuMetGlnPhe-GlyAspArgGluPheTyrArgAs 363
Db 241 TCTGCTCGTAATGCGCGTGGCTGACCTCATGCGAGTTGGGAGACCGGAGTTCTACCGGGA 300
Qy 363 pTTPTrpAsnSerGluSerValThrTyrPhe---TrpGlnAsnTrpAsnIleProVal 381
Db 301 CTGGGGGAATTCGACAGTGTGTTCACCTAATTCTGGGACAGAACTGGGAACATCCCTGTG 360
Qy 382 -HisLysTrpCysIleArg-HisPheTyrLysPheMetLeuArgGlySerSerLys 400
Db 361 GCACAGTGTGTGATTCATGACCAATTTTAAAGCCCAAGTTTCAGMGGGGACAGACGAA 420
Qy 401 TrpMetAlaArg 404
Db 421 TTGATGACGACG 432

RESULT 6
ABV83985
ID ABV83985 standard; cDNA; 433 BP.
XX
AC ABV83985;
XX
DT 09-DEC-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 314.
XX
KW Human; noctropic; neuroprotective; cytostratic; dermatological; vitruclide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antischistosis; antianaemic; antichitric; cancer;
KW antineumatic; hepatotropic; cerebroprotective; antinflammatory;
KW antifungal; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine;
KW gene; BG.
XX
OS Homo sapiens.
XX
PN US2002090672-A1.
XX
PD 11-JUL-2002.
XX
PF 17-JAN-2001; 2001US-00764853.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 11-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 14-JUL-2000; 2000US-0217496P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0226868P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0228287P.
PR 01-SEP-2000; 2000US-0228343P.
PR 01-SEP-2000; 2000US-0228344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.

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PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.

XX
PA (ROSE/) ROSEN C A.
PA (RUBEN/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
DR WPI, 2002-681727/73.
DR P-PDB; ABP67013.
XX
PT Novel polypeptide useful for diagnosis, prognosis, prevention, and
PT treatment of immune, hyperproliferative, renal, respiratory,
PT cardiovascular, reproductive, endocrine, gastrointestinal and
PT neurological disorders.
XX
PS Claim 1; SEQ ID NO 314; 369pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABV83682-ABV84101) and proteins
CC (ABP66710-ABP67129) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
SQ Sequence 433 BP; 87 A; 128 C; 111 G; 103 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.: 6,04e-48
Score: 603.50
Percent Similarity: 87.2%
Best Local Similarity: 85.1%
Query Match: 23.3%
DB: 6 Gaps: 1

US-10-659-800-6 (1-488) x ABV83985 (1-433)
Qy 264 GluLeuAenPheProArgSerProArgIleArgLysArgPheLeuArgArgIleLeu 283

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PD 17-APR-2003.
 XX 30-JUL-2001; 2001US-00918995.
 PF 30-JUL-2001; 2001US-00918995.
 PR 30-JUL-2001; 2001US-00918995.
 XX (DRMA/) DRMANC R T.
 XX (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX WPI; 2003-615964/58.
 DR New polynucleotide sequences obtained from various cDNA libraries, useful
 XX as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 PS Claim 1; SEQ ID NO 1979; 44pp; English.
 XX The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC segdata.uspto.gov/sequence.html?docID=20030073623
 CC
 SQ Sequence 471 BP; 78 A; 130 C; 153 G; 101 T; 0 U; 9 Other;
 Alignment Scores:
 Pred. No.: 4,946-22 Length: 471
 Score: 332.00 Matches: 71
 Percent Similarity: 53.4% Conservative: 0
 Best Local Similarity: 53.4% Mismatches: 2
 Query Match: 12.8% Indels: 62
 DB: Gaps: 2
 US-10-659-800-6 (1-488) x ACH14767 (1-471)
 QY 315 AepTYRSeRArgIleIleGluArgLeuLeuYleuA1a----- 327
 DB 58 GACCTACTACGCGATCATGACGGCCTCTCGAAGCTGGC-GGAGAAGCGGACAGGCGG 116
 QY 327 ----- 327
 DB 117 CATGCACAGACAGAGGAGGACAGTGGCAGTGGGAGAGTTCAGACTTGTGCGCA 176
 QY 328 -----ValProAsnHisLeuIleTPTLeuIlePhePheTyrTTPLeu 341
 DB 177 CCCCACACTCCCTGCGCAGGTCCCAATCACTCACTTGGCTATCTTCTTACTGGCTC 236
 QY 342 PheHisSerCyLeuAsnAlaValAlaGluLeuMetGlnPheGlyAspArgGluPheTyr 361
 DB 227 TTTCATCTCTGCGCTGAATGCGCTGTGATGCTCAATGACGTTTGGAGACCGGAGTTTCAAC 296
 QY 362 ArgAspTPTTTPAsn----- 366
 DB 297 CGGAGCTGTGTGTG-AGTGTCCCTGGGGGTGTCCTGGGGGCTGGAGATGGGCCATGTGTG 355

QY 367 -----SergIuSerValThrTyrPheTTP 374
 DB 356 CTCGTATCCCTCGTNGTCTCTTGCCCGCAGAGACTCGAGTCTGTCACTTCTCG 415
 QY 375 GlnAsnTTPAsnIleProValHisIleYstTPCyG1leArg 387
 DB 416 CAGAACTGGAACTCCCTGTGACACAGTGTGCATCAGG 454
 RESULT 9
 ABQ85322
 ID ABQ85322 standard; DNA; 380 BP.
 XX ABQ85322;
 AC 05-SEP-2002 (first entry)
 DT 05-SEP-2002 (first entry)
 XX Arabidopsis thaliana expressed polynucleotide SEQ ID NO 192.
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 192.
 XX Plant; Arabidopsis; transgenic; fungicide; insecticide; ds.
 KW Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX US2002062014-A1.
 PN 23-MAY-2002.
 PD 26-JAN-2001; 2001US-00770791.
 PF 27-JAN-2000; 2000US-0178480P.
 PR (GORL/) GORLACH J.
 XX (ANY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHEN A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRICK/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALIE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 XX Goriach J, An Y, Hamilton CM, Price J, Raines TM, Yu Y;
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 DR WPI; 2002-479265/51.
 XX New nucleic acid sequences of Arabidopsis thaliana and their encoded
 PT products are useful to produce transgenic plants, to screen for
 PT biologically active agents such as fungicides and insecticides and in
 PT genetic studies.
 PS Claim 1; SEQ ID NO 192; 18pp + Sequence Listing; English.
 XX The invention relates to a novel nucleic acid of Arabidopsis thaliana
 CC comprising a sequence capable of hybridising under stringency to one of
 CC the 999 sequences referred to but not defined in the specification
 CC (ABQ85331-ABQ86129). The nucleic acid sequences are useful to identify
 CC homologous or related genes, to produce compositions that modulate
 CC expression or function of the encoded protein, to map functional regions
 CC of the protein, to study associated physiological pathways, to
 CC genetically manipulate cells and plants. The encoded products are useful
 CC to screen for biologically active agents such as fungicides or

PF 12-APR-2000; 2000MO-US009696.
XX
XX 12-APR-1999; 99US-0128995P.
XX
XX (MONS) MONSANTO CO.
PA Venkatamesh M, Corbin DR, Bhat GB, Boddupalli SS, Grebenok RJ,
PI Kishore GM, Lardizabal KD, Laessner MW, Rangwala SH, Karunanandaa B,
XX WPI; 2000-665136/64.
XX
XX Genetically engineering the biosynthetic pathways in plants involved in
PT the accumulation of sterol compounds and tocopherol to produce compounds
PT for lowering the level of low density lipoprotein cholesterol in blood
PT serum.
XX
XX Disclosure; Page 62-63; 166pp; English.
XX
XX The present sequence is that of mouse acyl CoA:cholesterol
CC acyltransferase (ACAT) expressed sequence tag (EST) DNA sequence 11.
CC Mouse ACAT EST DNA sequence 1 is given in AAA88844. Sterol O-
CC acyltransferases such as ACAT catalyse the formation of cholesterol
CC esters from cholesterol and long chain fatty acids. Recombinant
CC constructs of the invention are used to alter the biosynthesis and
CC accumulation of sterols and tocopherols in transgenic plants. Seeds of
CC such plants may contain elevated levels of sitosterol and/or its esters,
CC and alpha-tocopherol, and reduced levels of campesterol and campestanol
CC and their esters. The seeds may also contain the novel sterol
CC brassicasteranol. Oil obtained from the seeds can be used in food and
CC pharmaceutical compositions to lower levels of low density lipoprotein
CC cholesterol in blood serum. ACAT enzymes can be used in the present
CC invention to produce elevated levels of phyosterol and/or phytosterol
CC esters
XX
XX SQ Sequence 299 BP; 50 A; 89 C; 85 G; 75 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.53e-13 Length: 299
Score: 232.00 Matches: 44
Percent Similarity: 96.1% Conservative: 5
Best Local Similarity: 86.3% Mismatches: 2
Query Match: 8.9% Indels: 1
DB: 3 Gaps: 0

US-10-659-800-6 (1-488) x AAA88845 (1-299)
QY 434 MetMetcAlaGlnIleProLeuAlaTrpPheValGlyArgPheGlnGlyAsnTyrgly 453
Db 3 ATGATGGCTCAAGTCCCACTGGCTGGATTTGGGCGCGATCTCTCCAGGGAACATATGCG 62
QY 454 AsnAlaValAlaTrpLeuSerLeuIleIleGlyGlnProIleAlaValLeuMetTyrgly 473
Db 63 AATGACGCTGTGGGTGACACTCATCATCTGGGCAACCGGTGGCTGT-CTCATGTATATGC 121
QY 474 HisAspTyrglyValLeuAsnTyrglyAlaPro 484
Db 122 CACGACTACTACTGTCTCACTACATGATGCCCA 154

RESULT 12
ADU81175
ID ADU81175 standard; cDNA; 400 BP.
XX
XX AC ADU81175;
XX
XX 10-FEB-2005 (first entry)
XX
XX Ryegrass diacylglycerol acyltransferase, DGAT, predicted cDNA.
XX
XX diacylglycerol acyltransferase; DGAT; plant breeding; crop improvement;
XX fatty acid biosynthesis; ss.
XX
XX Lolium perenne.
XX

PN WO20040101793-A1.
XX
XX PD 25-NOV-2004.
XX
XX PF 14-MAY-2004; 2004WO-AU000635.
XX
XX PR 16-MAY-2003; 2003AU-00902413.
XX
XX PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX
XX PA (AGRE-) AGRERESEARCH LTD.
XX
XX PI Bryan GT, Burling ME, Roberts NJ, Trollope AJ, Woodfield DR;
XX WPI; 2004-821891/81.
XX
XX PT New nucleic acid from a ryegrass (Lolium) or fescue (Festuca) species
PT encoding a diacylglycerol acyltransferase 1 (DGAT1) or DGAT1-like
PT polypeptide, useful as a genetic marker or for modifying fatty acid
PT biosynthesis in a plant.
XX
XX PS Example 1; SEQ ID NO 38; 188pp; English.
XX
XX CC The invention relates to a new substantially purified or isolated nucleic
CC acid or its fragment from a ryegrass (Lolium) or fescue (Festuca) species
CC encodes a diacylglycerol acyltransferase 1 (DGAT1) or DGAT1-like
CC polypeptide or its fragment or variant. The nucleic acid or nucleic acid
CC fragment and/or its nucleotide sequence information or single nucleotide
CC polymorphism of perennial ryegrass Lolium perenne is useful as a
CC molecular genetic marker or for modifying fatty acid biosynthesis in a
CC plant. The present sequence represents a plant diacylglycerol
CC acyltransferase, DGAT, cDNA.
XX
XX SQ Sequence 400 BP; 91 A; 85 C; 93 G; 131 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.05e-11 Length: 400
Score: 222.50 Matches: 51
Percent Similarity: 50.8% Conservative: 15
Best Local Similarity: 39.2% Mismatches: 40
Query Match: 8.6% Indels: 25
DB: 13 Gaps: 3

US-10-659-800-6 (1-488) x ADU81175 (1-400)
QY 373 PheTrpGlnAsnTrpAsnIleProValHisValTrpCyHisArgHisPheTyrglyPro 392
Db 1 TACTGAGAGATGTGGAAATATGCTGTGCAATATGAGTGTTCGCCATATATATTTCCC 60
QY 393 MetLeuArgArgGlySerSerIleTrpMetAlaArgThrGlyValPheLeuAlaSerAla 412
Db 61 CCCAGGCGCAGTGTATATCAAGAAGATGCTGCTTTGTATCATTTTGTATCTGCC 120
QY 413 PhePheHisGlyTyrLeuValSerValProLeuArgMetPheArgLeuTrpAlaPheThr 432
Db 121 GTGCTCCATGATGATTATGTTGCTGCTGCCCGCAATGTTCAGAGTTCCGGGCATTCTTA 180
QY 433 GlyMetMetAlaGlnIleProLeu-----AlaTrpPheValGlyArgPhePhe 448
Db 181 GGGATCATGTGCACATCCCTTTTATCATATTGACATCATCTTAAGCAAAATTCAGA 240
QY 449 GlnGlyAsnTyrglyAsnAlaValAlaValTrp----- 458
Db 241 GATACATATGGCCGGAACATGATATTCGTCTTTCTTCGATCTAGGACAGCCTATG 300
QY 459 -----LeuSerLeuIleIleGlyGlnProIleAlaValLeu 470
Db 301 CCGGCAATGATATTCTGTTCTTTCTTCG-ATCTACGACACGCTATGTGCGTTCTC 359
QY 471 MetTyrglyHisAspTyrglyValLeuAsn 480
Db 360 CTGTACTACCATGAT-----GTGATGAT 383

RESULT 13

ACH92522/c
ID ACH92522 standard; DNA; 121 BP.
XX
AC ACH92522;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon probe #25717.
XX
KW Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX
PD 16-OCT-2003.
XX
PF 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
PI Penn SG, Rank DR, Hanzel DK;
XX
DR WPI; 2004-119264/12.
XX
PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
PS Claim 1; SEQ ID NO 25717; 80bp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 688 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridizes under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX a method of selling and/or licensing single exon probes or microarrays to
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subscription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above. The probe, methods and apparatus are useful in gene
XX expression analysis. The probes may be used as tools for surveying
XX tissues to detect the presence of expressed messages that contain their
XX specific exon, or in constructing genome-derived single exon microarrays.
XX In addition, the probes are used in identifying and characterizing
XX alternative splicing events, in detecting and characterizing gross
XX alterations in the genomic locus that includes their exon, in assessing
XX smaller genomic alterations, in priming the synthesis of nucleic acids,
XX or in expressing the ORF-encoded peptide. The present sequence is a human
XX single exon probe of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from USPTO at
XX segdata.uspto.gov/sequence.html?DocID=20030194704

SQL Sequence 121 BP; 27 A; 30 C; 39 G; 25 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6,14e-12 Length: 121
Score: 217.00 Matches: 40
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 8.4% Indels: 0
DB: 12 Gaps: 0
US-10-659-800-6 (1-488) x ACH92522 (1-121)
QY 445 GlyArgPhePheGinglyAsnTyrglyAsnAlaAlaValTyrPleuSerLeuIleIleGly 464
DB 121 GCGCGCTTTTTCAGGGCACTATGCAACGACGCTGTGCTGTCCGTCATCATCGGA 62
QY 465 GlnProIleAlaValLeuMetTyrglyValHisAspTyrrTyrrValLeuAsnTyrglyAlaPro 484
DB 61 CAGCCATATGCGCGCTCATGTATGCTCCAGCATATCATGCTCATATGAGGCCCA 2
RESULT 14
AAD40442
ID AAD40442 standard; DNA; 400 BP.
AC AAD40442;
XX
XX 22-OCT-2002 (first entry)
XX
XX Bovine diacylglycerol acyltransferase (DGAT1) gene, Q allele.
XX
XX Bovine; diacylglycerol acyltransferase; genotyping; milk production;
KW DGAT1; polymorphism; farming industry; transgenic; enzyme; gene; de.
XX
XX Bos taurus.
XX
XX Key Location/Qualifiers
FH primer_bind complement(27..46)
FT /tag= a
FT /bound_moiety= "DGAT1.23"
FT primer_bind complement(225..244)
FT /tag= b
FT /bound_moiety= "DGAT1 11"
FT primer_bind 243..264
FT /tag= c
FT /bound_moiety= "DGAT1 14B"
FT primer_bind 379..400
FT /tag= d
FT /bound_moiety= "DGAT1 12"
XX
XX WO200236824-A1.
XX
XX 10-MAY-2002.
XX
XX 31-OCT-2001; 2001WO-NZ000245.
XX
XX 31-OCT-2000; 2000NZ-00507888.
XX
XX 06-DEC-2000; 2000NZ-00508652.
XX
XX (GEOR/) GEORGES M A J.
XX (COPP/) COPPIETERS W H R.
XX (GRIS/) GRISART B M J.
XX (SNEI/) SNEEL R G.
XX (REID/) REID S J.
XX (FORD/) FORD C A.
XX (SPEL/) SPELMAN R J.
XX
XX Georges MAJ, Coppieters WHR, Grisart BMJ, Snell RG, Reid SJ;
PI Ford CA, Spelman RJ;
XX
XX WPI; 2002-500128/53.
XX
XX Determining genetic merit of a bovine with respect to milk composition
PT and volume for improved milk production, comprises determining the

Qy	101	AlaArgLeuPheLeuGluAsnLeuIle	LeuTyrGlyIleLeuValAspProIleGlnVal	120
Db	251	GGACCGCTGGCACTTGAAATGTGATCAAAATATGATTTGATTAACACCCCTTCAGTGG		310
Qy	121	ValSerLeuPheLeuLysAspProH18-----SerTrpProAlaProCysLeuVal		137
Db	311	ATCTCAACGTTGTGGACATCATCAATTTGGAGCTGGCAAAATCTTGCTCTCATC		370
Qy	138	IleAlaIle		140
Db	371	CTATGCTCA		379

Search completed: May 6, 2006, 22:12:35
 Job time : 1371 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search using (frame plus p2n model)

Run on: May 7, 2006, 02:34:18 ; Search time 7600 Seconds
(without alignments)
5474.922 Million cell updates/sec

Title: US-10-659-800-6
Perfect score: 2594
Sequence: 1 MDRGSSRRRTGSRPSHG.....VLMYVDYVLYVEAPAAEA 488

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 6077154

Minimum DB seq length: 0
Maximum DB seq length: 500

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

MODEL=frame.p2n.model -DEV=xlh
-O=/abs/ABSWEB/spool/US10659800/runat_05052006_122306_17192/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.szlm500.rge -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=500
-HOST=abs6803h -USER=US10659800 @CGN 1.1 4939 @runat_05052006_122306_17192
-NCPUB=6 -ICPU=3 -NO MMAP -NEG_SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_da:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_srs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hlg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	842	32.5	452	6	CQ461886 Sequence
2	612	23.6	371	6	CQ463116 Sequence
3	367	14.1	201	10	BV207924 sqmm22493

4	352	13.6	201	10	BV207926	BV207926 sqmm22493
5	232	8.9	299	6	BD241855	BD241855 Acyl CoA:
6	232	8.9	299	6	AR227750	AR227750 Sequence
7	232	8.9	299	6	AX090338	AX090338 Sequence
8	197.5	7.6	381	6	BD241860	BD241860 Acyl CoA:
9	197.5	7.6	381	6	AR227755	BD118287 EST and e
10	176	6.8	113	6	BD118287	BD118287 Sequence
11	176	6.8	113	6	AR422734	AX983428 Sequence
12	176	6.8	113	6	AX983428	BD241847 Acyl CoA:
13	170	6.6	275	6	BD241847	AR227742 Sequence
14	170	6.6	275	6	AR227742	AX090352 Sequence
15	170	6.6	275	6	AX090352	BV102527 MARC 1757
16	168	6.5	310	10	BV102527	AR121924 Sequence
17	164	6.3	225	6	AR121924	BD223360 Toxicolog
18	164	6.3	225	6	BD223360	BD241846 Acyl CoA:
19	159	6.1	421	6	AX379068	AX379068 Sequence
20	155	6.0	253	6	BD241849	BD241849 Acyl CoA:
21	155	6.0	253	6	AR227744	AX090354 Sequence
22	155	6.0	253	6	AX090354	CQ923373 Sequence
23	143.5	5.5	386	6	CQ923373	BD241846 Acyl CoA:
24	127	4.9	267	6	BD241846	AR227741 Sequence
25	127	4.9	267	6	AR227741	AX090351 Sequence
26	127	4.9	267	6	AX090351	BD241845 Acyl CoA:
27	123.5	4.8	234	6	BD241845	AR227740 Sequence
28	123.5	4.8	234	6	AR227740	AX090350 Sequence
29	123.5	4.8	234	6	AX090350	AR672183 Sequence
30	103	4.0	200	6	AR672183	CQ532056 Sequence
31	101	3.9	65	6	CQ532056	CQ556741 Sequence
32	100	3.9	65	6	CQ556741	AF31513 Homo sapi
33	97	3.7	129	8	F331502S12	BV422477 S229P69FF
34	97	3.7	129	8	BV422477	CQ675847 Sequence
35	94	3.6	430	6	CQ675847	CQ051475 Sequence
36	91	3.5	471	6	CQ051475	CQ066524 Sequence
37	91	3.5	471	6	CQ066524	CQ093572 Sequence
38	91	3.5	471	6	CQ093572	CQ132342 Sequence
39	91	3.5	471	6	CQ132342	CQ170912 Sequence
40	91	3.5	471	6	CQ170912	CQ200059 Sequence
41	91	3.5	471	6	CQ200059	CQ215540 Sequence
42	91	3.5	471	6	CQ215540	CQ254134 Sequence
43	91	3.5	471	6	CQ254134	CQ291147 Sequence
44	91	3.5	471	6	CQ291147	CQ328262 Sequence
45	91	3.5	471	6	CQ328262	

ALIGNMENTS

RESULT 1
LOCUS CQ461886 452 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 4664 from Patent WO0192581.
ACCESSION CQ461886
VERSION CQ461886.1 GI:41427505
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Cnidaria; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1
Algate, P.A., Harlocker, S.L. and Jones, R.
Compositions and methods for the therapy and diagnosis of
ovarian cancer
Patent: WO 0192581-A 4664 06-DEC-2001.
JOURNAL CORIXA CORPORATION (US)
FEATURES
source
1..452
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 2.1e-54 Length: 452
Pred. No.: 452

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 14.1% Indels: 0
DB: 10 Gaps: 0
US-10-659-800-6 (1-488) x BV207924 (1-201)

QY 380 ProValHisLysLeuTrpCysIleArgHisPheTyrLysProMetLeuArgHisGlySerSer 399
DB 3 CCGTGCAACAAGTGGTGCATGACACCTCTCAAGCCCATGCTTGCAGCGGGCAGAC 62

QY 400 LysTrpMetAlaArgThrGlyValPheLeuAlaSerAlaPhePheHisGlyTyrLeuVal 419
DB 63 AAGTGATGGCCAGGACAGGGGGTGTCTCGGCTCGCTCTTCCACAGATCCAGTGGT 122

QY 420 SetValProLeuArgMetPheArgLeuTrpAlaPheThrGlyMetMetAlaGlnIlePro 439
DB 123 AGCGTCCCTCTCGAATGTTCCGCTCTGGGCGTTTCAAGGCAATGATGCTCAGATCCA 182

QY 440 LeuAlaTrpPheValGly 445
DB 183 CTGGCTGGTTCGTGGC 200

RESULT 4
BV207926 201 bp DNA linear STS 10-JUN-2004
LOCUS sqm224934 Human DNA (Sequenc) Homo sapiens STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV207926
VERSION BV207926.1 GI:48178556
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 201)
AUTHORS Nelson,R.M., Marellos,G., Kammerer,S., Hoyai,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
TITLE Large-scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
JOURNAL Genome Res. (2004) In press
COMMENT Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS Size: 201.
FEATURES
source Location/Qualifiers
1..201
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Human DNA (Sequenc)"
<1..>201
ORIGIN
STS
Alignment Scores:
Pred. No.: 4.56e-18 Length: 201
Score: 352.00 Matches: 66
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 13.6% Indels: 0
DB: 10 Gaps: 0
US-10-659-800-6 (1-488) x BV207926 (1-201)

QY 398 SerSerLysTrpMetAlaArgThrGlyValPheLeuAlaSerAlaPhePheHisGlyTyr 417
|||||

DB 3 AGCAGCAAGTGATGGCCAGGACAGGGGTGTTCTTGCCCTCGCCCTCTTCCACGAGTAC 62
QY 418 LeuValSerValProLeuArgMetPheArgLeuTrpAlaPheThrGlyMetMetAlaGln 437
DB 63 CTGGTAGGCTCCCTCTGGAATGTTCCGCTCTGGGCKTTACAGGGCAATGATGGCTCAG 122

QY 438 IleProLeuAlaTrpPheValGlyArgPhePheGlnGlyAsnTyrGlyAsnAlaAlaVal 457
DB 123 ATCCCACTGGCTGGTTCGTGGCGCGCTTTTCCAGGGCACTATAGCAACGACGCTG 182

QY 458 TrpLeuSerLeuIleIle 463
DB 183 TGGCTGCGCTCATCATC 200

RESULT 5
BD241855 299 bp DNA linear PAT 17-JUL-2003
LOCUS BD241855
DEFINITION Acyl CoA:cholesterol acyltransferase related nucleic acid
sequences.
ACCESSION BD241855
VERSION BD241855.1 GI:33051625
KEYWORDS JP 2002517201-A/12.
SOURCE Mus sp.
MUS sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 299)
AUTHORS Lasener,M.W. and Ruezinsky,D.M.
TITLE Acyl CoA:cholesterol acyltransferase related nucleic acid sequences
JOURNAL Patent: JP 2002517201-A 12 18-JUN-2002;
CALGENE LLC
COMMENT OS Mus sp. (murine)
PN JP 2002517201-A/12
PD 18-JUN-2002
PF 04-JUN-1999 JP 2000552290
PR 05-JUN-1998 US 60/088143, 12-NOV-1998 US 60/108389 PI
MICHAEL W LASNER, DIANE M RUEZINSKY
PC C12N15/09, A01HS/00, C11B1/00, C11C3/00, C12N1/21, C12N5/10, C12N9/
PC 10, C12N15/00,
PC C12N5/00
CC Acyl CoA:cholesterol acyltransferase related nucleic acid CC
FH Key Location/Qualifiers
FT source 1..299
FT Location/Qualifiers
1..299
/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
FEATURES
source Location/Qualifiers
1..299
/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
ORIGIN
Alignment Scores:
Pred. No.: 7.75e-09 Length: 299
Score: 232.00 Matches: 44
Percent Similarity: 96.1% Conservative: 5
Best Local Similarity: 86.3% Mismatches: 2
Query Match: 8.9% Indels: 1
DB: 6 Gaps: 0
US-10-659-800-6 (1-488) x BD241855 (1-299)

QY 434 MetMetAlaGlnIleProLeuAlaTrpPheValGlyArgPhePheGlnGlyAsnTyrGly 453
DB 3 ATGATGGCTCGAGTCCCGCTGGCTGTGTGGGCCCATTTCTCAAGGAACTATGGC 62

QY 454 AsnAlaAlaValTrpLeuSerLeuIleIleGlyGlnProIleAlaValLeuMetTyrVal 473
DB 63 AATGCACTGTGTGGGTACACTCATCTTGTGGCAACGGGTGGCTGT-CTCATGTATGTC 121
|||||

QY 474 HisAspTyrTrpValLeuAsnTyrGlnAlaPro 484
|||||

Db 122 CACGACTACTAGCTGCTCACTACGATGCCCA 154

RESULT 6 AR227750 AR227750 299 bp DNA linear PAT 20-DEC-2002

LOCUS AR227750 Sequence 13 from patent US 6444876.

DEFINITION AR227750

ACCESSION AR227750

VERSION AR227750.1 GI:27266341

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 299)

AUTHORS Laessner,M.W. and Ruezinsky,D.M.

TITLE Acyl CoA: cholesterol acyltransferase related nucleic acid sequences

JOURNAL Patent: US 6444876-A 13 03-SEP-2002;

Calgene LLC; Davis, CA;

MOX:

FEATURES

Location/Qualifiers

1..299

/organism="Unknown"

/mol_type="Genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.75e-09 Length: 299

Score: 232.00 Matches: 44

Percent Similarity: 96.1% Conservative: 5

Best Local Similarity: 86.3% Mismatches: 2

Query Match: 8.9% Indels: 1

Gaps: 0

US-10-659-800-6 (1-488) x AR227750 (1-299)

Qy 434 MetMetAlaGlnIleProLeuAlaTrpPheValGlyArgPheGlnGlyAsnTyrGly 453

Db 3 ATGATGGCTCAGGTCCTCCACTGGCTGATGTGGGCCGATCTCTCCAGGGAACATATGCG 62

Qy 454 AsnAlaAlaValaTrpLeuSerLeuIleIleGlyGlnProIleAlaValLeuMetTyrVal 473

Db 63 AATGACGCTGTGGTGTCACACTCATCTGAGCAACCGGTGGCTGT-CTCATGTATGTC 121

Qy 474 HisAepTyrTyrValLeuAsnTyrGlnAlaPro 484

Db 122 CACGACTACTAGCTGCTCACTACGATGCCCA 154

RESULT 7 AX090338 299 bp DNA linear PAT 21-MAR-2001

LOCUS AX090338 Sequence 31 from Patent WO0116308.

DEFINITION AX090338

ACCESSION AX090338

VERSION AX090338.1 GI:13444204

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Laessner,M. and van Bennekom,A.

TITLE Plant sterol acyltransferases

JOURNAL Patent: WO 0116308-A 31 08-MAR-2001;

MONSANTO COMPANY (US)

FEATURES

Location/Qualifiers

1..299

/organism="Mus musculus"

/mol_type="unassigned DNA"

/db_xref="taxon:10090"

ORIGIN

Alignment Scores:

Pred. No.: 7.75e-09 Length: 299

Score: 232.00 Matches: 44

Percent Similarity: 96.1% Conservative: 5

Best Local Similarity: 86.3% Mismatches: 2

Query Match: 8.9% Indels: 1

Gaps: 0

US-10-659-800-6 (1-488) x AX090338 (1-299)

Qy 434 MetMetAlaGlnIleProLeuAlaTrpPheValGlyArgPheGlnGlyAsnTyrGly 453

Db 3 ATGATGGCTCAGGTCCTCCACTGGCTGATGTGGGCCGATCTCTCCAGGGAACATATGCG 62

Qy 454 AsnAlaAlaValaTrpLeuSerLeuIleIleGlyGlnProIleAlaValLeuMetTyrVal 473

Db 63 AATGACGCTGTGGTGTCACACTCATCTGAGCAACCGGTGGCTGT-CTCATGTATGTC 121

Qy 474 HisAepTyrTyrValLeuAsnTyrGlnAlaPro 484

Db 122 CACGACTACTAGCTGCTCACTACGATGCCCA 154

RESULT 8 BD241860 381 bp DNA linear PAT 17-JUN-2003

LOCUS BD241860

DEFINITION BD241860

ACCESSION BD241860.1 GI:33051630

VERSION BD241860

KEYWORDS JP 2002517201-A/17.

SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Pelodierinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 381)

AUTHORS Laessner,M.W. and Ruezinsky,D.M.

TITLE Acyl CoA: cholesterol acyltransferase related nucleic acid sequences

JOURNAL Patent: JP 2002517201-A 17 18-JUN-2002;

CALGENE LLC

COMMENT OS Caenorhabditis elegans (nematode)

PN JP 2002517201-A/17

PD 18-JUN-2002

PF 04-JUN-1999 JP 2000552290

PR 05-JUN-1998 US 60/088143 12-NOV-1998 US 60/108389 PI

MICHAEL W LASSNER, DIANE M RUEZINSKY

PC C12N15/09,A01H5/00,C11B1/00,C11C3/00,C12N1/21,C12N5/10,C12N9/

PC 10,C12N5/00,

PC C12N5/00

CC n ac position 46 is unknown

CC key Location/Qualifiers

FT misc_feature (46).

FEATURES

Location/Qualifiers

1..381

/organism="Caenorhabditis elegans"

/mol_type="Genomic DNA"

/db_xref="taxon:6239"

ORIGIN

Alignment Scores:

Pred. No.: 4.11e-06 Length: 381

Score: 197.50 Matches: 41

Percent Similarity: 91.2% Conservative: 22

Best Local Similarity: 39.8% Mismatches: 31

Query Match: 7.6% Indels: 9

Gaps: 2

US-10-659-800-6 (1-488) x BD241860 (1-381)

Qy 47 ProAlaProAlaProAsn-----LysAepGlyAepAlaGlyValGly 60

Db 71 CCAAGTACGCTCCCTCATATTGCACAAAATGTAATTCCTCAAGGGAAGTTCAAGAAATG 130

Qy 61 SerGlyHisTrpGlnLeuArgCysHisArgLeuGlnAepSerLeuPheSerSerAspSer 80

Db 131 AGAGGACCTTGCAGAAAGTGTACATACCTGCTCAAGATTCATTGTTTTCACAGACTTCT 190

QY 81 GlyPheSerAsnTyrArgGlyIleLeuAsnTrpCysValIleMetLeuIleuSerAsn 100
DB 191 GGATGACAAATTTCCGCGGATTCCTTCATTTGCTCAATTTTCTTGGTACTTCAAAAT 250
QY 101 AlaArgLeuPheLeuGlnAsnLeuIleIleTyrGlyIleLeuValAspProIleGlnVal 120
DB 251 GGAACCGCGGACCTTGAAAATGTGATCAAAATATGATTTGATTAACACCCCTTCAGTGG 310
QY 121 ValSerLeuPheLeuLysAspProHis-----SerTrpProAlaProCysLeuVal 137
DB 311 ATCTCAAGCTTTGTGAGCATCATCACTCAATTTGAGCTGGCCAAATCTTCTCTCACC 370
QY 138 IleAlaIle 140
DB 371 CTATGCTCA 379

RESULT 9
AR227755 381 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 20 from patent US 6444876.
ACCESSION AR227755
VERSION AR227755.1 GI:27266346
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 381)
AUTHORS Laesher,M.W. and Ruezinsky,D.M.
TITLE Acyl CoA: cholesterol acyltransferase related nucleic acid sequences
JOURNAL Patent: US 6444876-A 20 03-SEP-2002;
Caigene LLC; Davis, CA;
WOX;

FEATURES
source Location/Qualifiers
1..381
/organism="Unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 4,11e-06 Length: 381
Score: 197.50 Matches: 41
Percent Similarity: 61.24 Conservative: 22
Best Local Similarity: 39.84 Mismatches: 31
Query Match: 7.6% Indels: 9
DB: 6 Gaps: 2

US-10-659-800-6 (1-488) x AR227755 (1-381)

QY 47 ProAlaProAlaProAsn-----LysAspGlyAspAlaGlyValGly 60
DB 71 CCGATGACGCTCCATTCATTTGCACAAATGTAAATTCGCAAGGAAAGTTTCAGAAATG 130
QY 61 SerGlyHisTrpGlyLeuArgCysHisArgLeuGlnAspSerLeuPheSerSerAspSer 80
DB 131 AGAGCACTTGGGACAAAGTGTACTACTGCTCAAGATTCATTTGTTTTCAGAGATTCT 190
QY 81 GlyPheSerAsnTyrArgGlyIleLeuAsnTrpCysValIleMetLeuIleuSerAsn 100
DB 191 GGATGACAAATTTCCGCGGATTCCTTCATTTGCTCAATTTTCTTGGTACTTCAAAAT 250
QY 101 AlaArgLeuPheLeuGlnAsnLeuIleIleTyrGlyIleLeuValAspProIleGlnVal 120
DB 251 GGAACCGCGGACCTTGAAAATGTGATCAAAATATGATTTGATTAACACCCCTTCAGTGG 310
QY 121 ValSerLeuPheLeuLysAspProHis-----SerTrpProAlaProCysLeuVal 137
DB 311 ATCTCAAGCTTTGTGAGCATCATCACTCAATTTGAGCTGGCCAAATCTTCTCTCACC 370
QY 138 IleAlaIle 140
DB 371 CTATGCTCA 379

RESULT 10
BD118287 113 bp DNA linear PAT 18-SEP-2002
LOCUS EST and encoded human protein.
DEFINITION BD118287
ACCESSION BD118287.1 GI:23213197
VERSION JP 2002010789-A/10364.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 113)
AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 10364 15-JAN-2002;
GENSET CORP

COMMENT
OS Homo sapiens (human)
PN JP 2002010789-A/10364
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC EST and encoded human protein
FH Key Location/Qualifiers
FT source 1..113
FT Location/Qualifiers
1..113
/organism="Homo sapiens"
/mol_type="genomic DNA"
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ORIGIN
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Score: 176.00 Matches: 36
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Query Match: 6.8% Indels: 1
DB: 6 Gaps: 0

US-10-659-800-6 (1-488) x BD118287 (1-113)

QY 417 TyrLeuValSerValProLeuArgMetPheArgLeuTrpAlaPheThrGlyMetMetAla 436
DB 3 TACCTGGAGACGCTCCCTCTGCGAATGTTCCGCTCTGGG-TTCACGGGCATGATGCT 61
QY 437 GlnIleProLeuAlaTrpPheValGlyTyrPhePheGlnGlyAsnTyrGly 453
DB 62 CAGATCCACCTGCGCTGCTGCTGCGCGCTTTTTCAGGGCACTATGCT 112

RESULT 11
AR422734 113 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 14231 from patent US 6639063.
DEFINITION AR422734
ACCESSION AR422734
VERSION AR422734.1 GI:40177844
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 113)
AUTHORS Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 14231 28-OCT-2003;
Genetec S.A.,;

MOX:

FEATURES

source

1.113

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 3,576-05 Length: 113

Score: 176.00 Matches: 36

Percent Similarity: 97.3% Conservative: 0

Best Local Similarity: 97.3% Mismatches: 1

Query Match: 6.8% Indels: 1

DB: 6 Gaps: 0

US-10-659-800-6 (1-488) x AR422734 (1-113)

OY 417 TyrluValSerValProleuArgMetPheArgLeuTrpAlaPheThrGlyMetMetAla 436

DB 3 TACCTGGTGAAGCGTCCCTCTCGGAAATGTTCCGCTCTGGGG-TTCACGGGCAATGAGCT 61

OY 437 GlnIleProLeuAlaTrpPheValGlyArgPhePheGlnGlyAsnTyrGly 453

DB 62 CAGATCCACACTGGCTGTTCCGTGGGCGCGCTTTTCCAGGGCAACTATGGC 112

RESULT 12

LOCUS AX983428 113 bp DNA linear PAT 15-JAN-2004

DEFINITION Sequence 14231 from Patent EP1104808.

ACCESSION AX983428

VERSION AX983428.1 GI:40989568

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 Dunas Mline Edwards,J.B., Jobert,S. and Giordano,J.Y.

AUTHORS

ESTs and encoded human proteins

TITLE

Patent: EP 1104808-A 14231 06-JUN-2001;

JOURNAL

Genset (FR)

FEATURES

source

1.113

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 3,576-05 Length: 113

Score: 176.00 Matches: 36

Percent Similarity: 97.3% Conservative: 0

Best Local Similarity: 97.3% Mismatches: 1

Query Match: 6.8% Indels: 1

DB: 6 Gaps: 0

US-10-659-800-6 (1-488) x AX983428 (1-113)

OY 417 TyrluValSerValProleuArgMetPheArgLeuTrpAlaPheThrGlyMetMetAla 436

DB 3 TACCTGGTGAAGCGTCCCTCTCGGAAATGTTCCGCTCTGGGG-TTCACGGGCAATGAGCT 61

OY 437 GlnIleProLeuAlaTrpPheValGlyArgPhePheGlnGlyAsnTyrGly 453

DB 62 CAGATCCACACTGGCTGTTCCGTGGGCGCGCTTTTCCAGGGCAACTATGGC 112

RESULT 13

LOCUS BD241847 275 bp DNA linear PAT 17-JUL-2003

DEFINITION Acyl CoA:cholesterol acyltransferase related nucleic acid sequences.

ACCESSION

BD241847

VERSION

BD241847.1 GI:33051617

KEYWORDS

JP 2002517201-A/4.

SOURCE

Glycine max (soybean)

ORGANISM

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroside I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

1 (bases 1 to 275)

AUTHORS

Laessner,M.W. and Ruezinsky,D.M.

TITLE

Acyl CoA:cholesterol acyltransferase related nucleic acid sequences

JOURNAL

Patent: JP 2002517201-A 4 18-JUN-2002;

COMMENT

CALGENE LLC

OS Glycine max (soybean)

PN JP 2002517201-A/4

PD 18-JUN-2002

PF 04-JUN-1999 JP 2000552290

PR 05-JUN-1998 US 60/088143,12-NOV-1998 US 60/108389 PI

MICHAEL W LAESSNER,DIANE M RUEZINSKY

PC C12N15/09,A01H5/00,C11B1/00,C11C3/00,C12N1/21,C12N5/10,C12N9/10,C12N5/00,

PC C12N5/00

CC n at positions 192, 202, 204, 211, 222, 234, 238, 239, 244,

CC 245, 247, 251,

CC 262, and 263 is unknown

CC Key Location/Qualifiers

FT misc feature (192)..(263).

FEATURES

source

1.275

/organism="Glycine max"

/mol_type="genomic DNA"

/db_xref="taxon:3847"

ORIGIN

Alignment Scores:

Pred. No.: 0.000315 Length: 275

Score: 170.00 Matches: 34

Percent Similarity: 62.7% Conservative: 13

Best Local Similarity: 45.3% Mismatches: 28

Query Match: 6.6% Indels: 1

DB: 6 Gaps: 0

US-10-659-800-6 (1-488) x BD241847 (1-275)

OY 365 TrpAenSerGluSerValThrTrpPheArgGlnAsnTrpAenIleProValIleYerTrp 384

DB 2 TGGATGCCAAACCTGTTGAAGATTTATGAGATGTGAATATCCCTGTACAAATGG 61

OY 385 CysIleArgHisPheTyrLysProMetLeuArgArgGlySerSerLysTrpMetAlaArg 404

DB 62 ATGATCCGCCACCTATATTTCATGTTAAAGCACGGTATACCAAGCCGCTCTT 121

OY 405 ThrGlyValPheLeuAlaSerValPhePheHisGluTyrTrleuValSerValProleuArg 424

DB 122 TTAATTCCTTCCTGGT-TCTGCTTATTTCCATGAGCTGTGCATCGCTGCTTGGCCA 180

OY 425 MetPheArgLeuTrpAlaPheThrGlyMetMetAlaGlnIlePro 439

DB 181 CATATTCAAGTNGGGGTTTNGNGAATTTAAGTTTCAGTNCCT 225

RESULT 14

LOCUS AR227742 275 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 5 from patent US 644876.

ACCESSION

AR227742

VERSION

AR227742.1 GI:27266333

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 275)

AUTHORS

Laessner,M.W. and Ruezinsky,D.M.

TITLE

Acyl CoA:cholesterol acyltransferase related nucleic acid

sequences
JOURNAL Patent: US 6444876-A 5 03-SEP-2002;
Calgene LLC; Davis, CA;
W01;

FEATURES
source Location/Qualifiers
1..275
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 0.000315 Length: 275
Score: 170.00 Matches: 34
Percent Similarity: 62.7% Conservative: 13
Best Local Similarity: 45.3% Mismatches: 28
Query Match: 6.6% Indels: 1
DB: 6 Gaps: 0

US-10-659-800-6 (1-488) x AR227742 (1-275)

Qy 365 TTPAenSerGluSerValThrTyrPheTrpGlnAenTrpAenIleProValHisIysTrp 384
Db 2 TGAATGCCAAACCTGTGAAGATTATGAGAGATGGAATATGCTGTTCACAAATGG 61
Qy 385 CysIleArgHisPheTyrLysProMetLeuArgGlySerSerIysTrpMetAlaArg 404
Db 62 ATGATCCGCCACCTATATTTTCCATGTTTAAGCAGCGTATACCAAGGCCGTCCTCTT 121
Qy 405 ThrGlyValPheLeuAlaSerAlaPhePheHisGlyTyrLeuValSerValProLeuArg 424
Db 122 TTAATTGCCCTTCCTGCT-TCTGCTTATTCATGAGCTGTCATGCTGCTGCTTGCCTCA 180
Qy 425 MetPheArgLeuTrpAlaPheThrGlyMetMetAlaGlnIlePro 439
Db 181 CATATTCAAGTNGTGGTTTCNGNGAATTAAGTTTCAAGTNCCT 225

RESULT 15

AX090352 275 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 45 from Patent W00116308.
DEFINITION AX090352
ACCESSION AX090352
VERSION AX090352.1 GI:13444213
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

1 Laessle, M. and van Eenennaam, A.
TITLE Plant sterol acyltransferases
JOURNAL Patent: WO 0116308-A 45 08-MAR-2001;
MONSANTO COMPANY (US)
FEATURES
source Location/Qualifiers
1..275
/organism="Glycine max"
/mol_type="unassigned DNA"
/db_xref="taxon:3847"
1..275
/note="n=unknown"

ORIGIN

Alignment Scores:
Pred. No.: 0.000315 Length: 275
Score: 170.00 Matches: 34
Percent Similarity: 62.7% Conservative: 13
Best Local Similarity: 45.3% Mismatches: 28
Query Match: 6.6% Indels: 1
DB: 6 Gaps: 0

US-10-659-800-6 (1-488) x AX090352 (1-275)

Qy 365 TTPAenSerGluSerValThrTyrPheTrpGlnAenTrpAenIleProValHisIysTrp 384
Db 2 TGAATGCCAAACCTGTGAAGATTATGAGAGATGGAATATGCTGTTCACAAATGG 61
Qy 385 CysIleArgHisPheTyrLysProMetLeuArgGlySerSerIysTrpMetAlaArg 404
Db 62 ATGATCCGCCACCTATATTTTCCATGTTTAAGCAGCGTATACCAAGGCCGTCCTCTT 121
Qy 405 ThrGlyValPheLeuAlaSerAlaPhePheHisGlyTyrLeuValSerValProLeuArg 424
Db 122 TTAATTGCCCTTCCTGCT-TCTGCTTATTCATGAGCTGTCATGCTGCTGCTTGCCTCA 180
Qy 425 MetPheArgLeuTrpAlaPheThrGlyMetMetAlaGlnIlePro 439
Db 181 CATATTCAAGTNGTGGTTTCNGNGAATTAAGTTTCAAGTNCCT 225

Search completed: May 7, 2006, 04:54:30
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GenCore version 5.1.8
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OM protein - nucleic search, using frame_p2n model

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Sequence: 1 MGDGRSSRRRTGSRPSSHG.....VLMYHDYVLYNPAEAAEA 488

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Ygapop 10.0, Ygapext 0.5
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Delop 6.0, Delext 7.0

Searched: 9306428 seqs, 203626586 residues
Total number of hits satisfying chosen parameters: 14491570

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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score greater than or equal to the score of the result being pinned,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

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3	149	5.7	201	10	US-10-995-561-13111	Sequence 13111, A
4	98	3.8	201	10	US-10-995-561-64752	Sequence 64752, A
5	96	3.7	201	10	US-10-995-561-64711	Sequence 64711, A
6	86	3.3	201	10	US-10-995-561-64750	Sequence 64750, A
7	83.5	3.2	444	13	US-10-993-809-47	Sequence 47, Appl
8	82.5	3.2	462	18	US-11-096-568A-12018	Sequence 12018, A
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19	78	3.0	442	12	US-10-301-480-321978	Sequence 321978,
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27	77.5	3.0	436	12	US-10-301-480-664716	Sequence 664716,
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30	77.5	3.0	489	7	US-09-925-065A-175339	Sequence 175339,
31	77.5	3.0	493	7	US-09-925-065A-137506	Sequence 137506,
32	77.5	3.0	493	7	US-09-925-065A-137507	Sequence 137507,
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35	77	3.0	487	17	US-11-108-172-140	Sequence 140, App
36	76.5	2.9	378	7	US-09-925-065A-86862	Sequence 86862, A
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38	76.5	2.9	378	12	US-10-301-480-801511	Sequence 801511,
39	76.5	2.9	387	13	US-10-496-351-44	Sequence 44, Appl
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41	75.5	2.9	319	7	US-09-925-065A-48873	Sequence 48873, A
42	75.5	2.9	319	11	US-10-301-480-150111	Sequence 150111,
43	75.5	2.9	196	12	US-10-301-480-763520	Sequence 763520,
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ALIGNMENTS

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; Sequence 13119, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARCILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13119
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13119
Alignment Scores: 6.77e-06 Length: 201
Pred. No.: 1

Score: 166.00 Matches: 30
Percent Similarity: 63.6% Conservative: 12
Best Local Similarity: 45.5% Mismatches: 22
Query Match: 6.4% Indels: 2
DB: 10 Gaps: 1

US-10-659-800-6 (1-488) x US-10-995-561-13119 (1-201)

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DB 3 CTACGATTTGGAGACAGATGTTCTACCGGAGCTGGTGAACCTCAACGCTCTTCCAC 62
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      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 63 TACTACCGCACTTGGACCTGGTGTGCTCATGACTGGCTTACGACTGACTGATATCAGAT 122
OY 393 MetLeuArg-----ArgGlySerSerIystrpMetAlaArgThrGlyValPheLeuAla 410
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 123 GGGGTGGCGGCTCTGTGTCGCCGGCCGAGGGGTAGCATCTGGGTGTGTTCCGTGTC 182
OY 411 SerAlaPhePheHisGlu 416
      ::::::::::::::::::
DB 183 TCCGCAGTGGCCCATGAG 200
```

RESULT 2

US-10-995-561-13118 Application US/10995561
; Sequence 13118, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13118
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13118

Alignment Scores:

Pred. No.: 8,17e-05 Length: 201
Score: 154.00 Matches: 25
Percent Similarity: 65.0% Conservative: 14
Best Local Similarity: 41.7% Mismatches: 21
Query Match: 5.9% Indels: 0
DB: 10 Gaps: 0

US-10-659-800-6 (1-488) x US-10-995-561-13118 (1-201)

```
OY 319 IleIleGluArgLeuLeuIleValProAsnHisLeuIleTrpLeuIlePhePhe 338
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 22 CTGGGCTCTCTATCTGTGATGCCAGTTCGACGAGCATTCATGCTGCTCATCTTC 81
OY 339 TyrTrpLeuPheHisSerCysLeuAsnAlaValAlaGluLeuMetGlnPheGlyAspArg 358
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 82 TTGGCTTCTCTCATGCTGCTCAACGCTTTGGCGAGATGCTACGATTTGGAGACAG 141
OY 359 GluPheTyrArgAspTrpTrpAsnSerGluSerValThrTyrPheTrpGlnAsnTrpAsn 378
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 142 ATGTTCTACCGGAGCTGAGGAACTCAACGCTCTTCTCAACTACTACCGCACTTGGAAC 201
```

RESULT 3

US-10-995-561-13111 Application US/10995561
; Sequence 13111, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13111
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13111

Alignment Scores:
Pred. No.: 0.000231 Length: 201
Score: 149.00 Matches: 27
Percent Similarity: 60.7% Conservative: 10
Best Local Similarity: 44.3% Mismatches: 22
Query Match: 5.7% Indels: 2
DB: 10 Gaps: 1

US-10-659-800-6 (1-488) x US-10-995-561-13111 (1-201)

```
OY 360 PheTyrArgAspTrpTrpAsnSerGluSerValThrTyrPheTrpGlnAsnTrpAsnIle 379
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 6 TTCTACCGGAGCTGAGGAACTCAACGCTCTTCTCAACTACTACCGCACTTGGAACTG 65
OY 380 ProValHisTyrTrpCy1IleArgHisPheTyrIysProMetLeuArg-----ArgGly 397
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 66 GTGTCCTACGACTGCTGTACAGCTGATCATGASATGAGGCTGGCGCTCTTGGTCC 125
OY 398 SerSerIystrpMetAlaArgThrGlyValPheLeuAlaSerAlaPhePheHisGluTyr 417
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 126 CGGGCCGAGGAGGTATGACATCTGGGTGTGTTCTCGTCTCGGACGTGCCCATGAGATAT 185
OY 418 Leu 418
      ::
DB 186 ATC 188
```

RESULT 4

US-10-995-561-64752 Application US/10995561
; Sequence 64752, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64752
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-64752

Alignment Scores:
Pred. No.: 9.11 Length: 201
Score: 98.00 Matches: 16
Percent Similarity: 56.8% Conservative: 9
Best Local Similarity: 36.4% Mismatches: 15
Query Match: 3.8% Indels: 4
DB: 10 Gaps: 1

US-10-659-800-6 (1-488) x US-10-995-561-64752 (1-201)

```
OY 362 ArgAspTrpTrpAsnSerGluSerValThrTyrPheTrpGlnAsnTrpAsnIleProVal 381
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 30 CAGGACTGTGAACTCAACGCTCTTCTCAACTACTACCGCACTTGGAACTGAGTGTGTC 89
```

[illegible]

RESULT 5

US-10-995-561-64711
; Sequence 64711; Application US/10995561
; Publication No. US20050272054A1

```

: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele et al.
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
: TITLE OF INVENTION: DETECTION AND USES THEREOF
: FILE REFERENCE: CL001559
: CURRENT APPLICATION NUMBER: US/10/995,561
: CURRENT FILING DATE: 2004-11-24
: NUMBER OF SEQ. ID NOS: 85702
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO 64711
: LENGTH: 201
: TYPE: DNA
: ORGANISM: Homo sapiens
: IS-10-995-561-64711

```

Alignment Scores:

Pred. No.:	13	8	length:	20
Score:	96.00		Matches:	16
Percent Similarity:	54.5%		Conservative:	8
Best Local Similarity:	36.4%		Mismatches:	16
Query Match:	3.7%		Indels:	
GB:	10		Gaps:	1

US-10-659-800-6 (1-488) x US-10-995-561-64711 (1-201)

```

Oy      362 ArgAspTyrTrpAsnSerGluSerValThrTyrPheTrpGlnAsnTrpAsnIleProVal 38U
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      12 CAGAGACTGGTGGAACTCAACGTCCTTCTCAACTACTACCGCACTTGGAACGCGTGC 71

```

```
Oy      362 HILVSTTPCYSLIETARGHSPHEITYLYLSPROMELCWAQYARGGLYSERLYSTTP 401
       ||| ||| :||| ||||| |||
Db      72 CATACTGGCTGTACAGCTACTGTATCASATGCGCTGCCG-----GTATGG 119
```

Qy	402	MetAlaArgThr	405
		:::	
Db	120	GCCCTGCAGACC	131

RESULT 6

US-10-995-561-64750
; Sequence 64750; Application US/10995561
; Publication No. US20050272054A1

```

: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele et al.
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
: TITLE OF INVENTION: DETECTION AND USES THEREOF
: FILE REFERENCE: CL001559
: CURRENT APPLICATION NUMBER: US/10/995,561
: CURRENT FILING DATE: 2004-11-24
: NUMBER OF SEQ. ID NOS: 85702
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO 64750
: LENGTH: 201
: TYPE: DNA
: ORGANISM: Homo sapiens
: IS-10-995-561-64750

```

Alignment Scores:

Pred. No.:	110	Length:	201
Score:	86.00	Matches:	16

```
Percent Similarity: 64.7%  Conservative: 6
Best Local Similarity: 47.1%  Mismatches: 1
Query Match: 3.3%  Indels: 0
DB: 10  Gaps: 0
```

US-10-659-800-6 (1-488) X US-10-995-561-64750 (1-201)

Oy 329 ProxsnHleuNietrPnHiePherPhYtTgrLeupRenIseCerGuysAuaPaLa 348
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 52 CCAAGCATTTTCATGCTGTCTACTATTCTTGCTCTCCATGCATGGTCTACAGGCC 111

Dy 349 ValAlaGluLeuMetGlnPheGlyAspArgGluPheTyrArg 362
|||:::|||
Db 112 TTGGCGAGATGCTACGATTGGAGACAGATGTCTACC GG 153

RESULT

US-10-983-809-47
; Sequence 47, Application US/10983809
; Publication No. US20060063164A1

```

: GENERAL INFORMATION:
: APPLICANT: An, Sungwhan
: APPLICANT: Yoon, ChiWang
: APPLICANT: Oh, Taejeong
: APPLICANT: Yoon, DaekYoung
: APPLICANT: Lee, SunWoo
: APPLICANT: Kim, MyungSoon
: APPLICANT: Woo, SukKyung
: TITLE OF INVENTION: METHOD FOR DETECTING METHYLATION OF PROMOTER USING RESTRICTION
: TITLE OF INVENTION: ENZYME AND DNA CHIP
: FILE REFERENCE: 4240-113
: CURRENT APPLICATION NUMBER: US/10/983,809
: CURRENT FILING DATE: 2004-11-08
: PRIOR APPLICATION NUMBER: KR 10-2004-0075395
: PRIOR FILING DATE: 2004-09-21
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO: 47
: LENGTH: 444
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-983-809-47

```

Alignment Scores:

Pred. No.:	465	Length:	44
Score:	83.50	Matches:	28
Percent Similarity:	47.2%	Conservative:	6
Best Local Similarity:	38.9%	Mismatches:	29
Query Match:	3.2%	Indels:	9
DB:	13	Gaps:	4

US-10-659-800-6 (1-488) x US-10-983-809-47 (1-444)

QY 2 GlyAspArgGlySerSerArg---ArgArgArgThrGlySerArgProSerSerHisGly 20

21 GlyGlyGlyProAlaAlaAlaGluGluGluValAlaArgAspAlaAlaAlaGlyProAspVal 40

41 GlyAlaAlaGlyAspAlaProAlaPro-----AlaProAlaGlyAspGly--- 55

Gy 56 -----AspAlaGlyValGlySerGlyHisTrpGlu 65
|||||
|||::|||

RESULT 8
US-11-096-568A-12018/c
; Sequence 12018, Application US/11096568A

Publication No. US20060048240A1
; GENERAL INFORMATION:


```
Qy 25 -----AlaAlaAlaGluGluGluValAlaArgAspAlaAlaAlaGlyProAspValAlaAla 42
Db 164 CCCACCGCGCGCCAGAGGAGAGAGAACCCGGGCGTCCGCCGAGCTTCGAGAGACGCG 243
Qy 43 AlAGlyAspAlaProAlaProAlaProAlaProAlaProAlaGlyAspAlaGlyValGlySerGly 62
Db 244 GCGCGGAGAGAGAGCGCGCGCGCGCGGAGCAACGCGCGCGCGGACAGAGCTCGGG 303
Qy 63 -----HisTrpGluLeuArgCysHisArgLeuGlnAspSerLeuPhe 76
Db 304 CCAAGCGCGCGCGCATCCCGCGCGCGCGCGGTGAGAGAGCTTGGCGGCTGCGGATG 363
Qy 77 SerSerAsp---SerGlyPheSerAspAntyTrArgGlyIleLeuAsnTrp 91
Db 364 CCCGAGACAGAGATGAGCAAAAGCAAGATGCGAGGATTTAGCTCG 411

RESULT 11
US-10-301-480-865431
; Sequence 865431, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIORITY FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1256818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 865431
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-865431

Alignment Scores:
Pred. No.: 798 Length: 452
Score: 81.00 Matches: 33
Percent Similarity: 36.5% Conservative: 2
Best Local Similarity: 34.4% Mismatches: 49
Query Match: 3.1% Indels: 12
Gaps: 4

US-10-659-800-6 (1-488) x US-10-301-480-865431 (1-452)
Qy 8 ArgArgArgArgThyGlySerArgProSer-----SerHisGlyGlyGlyGlyPro--- 24
Db 124 AGACGAGCAATACAGGCGCGCGCGCGCGAGCTGCATGTGACGGGCAAGCGGCCCTTT 183
Qy 25 -----AlaAlaAlaGluGluGluValAlaArgAspAlaAlaAlaGlyProAspValAlaAla 42
Db 184 CCCACCGCGCGCCAGAGGAGAGAGAACCCGGGCGTCCGCCGAGCTTCGAGAGACGCG 243
Qy 43 AlAGlyAspAlaProAlaProAlaProAlaProAlaProAlaGlyAspAlaGlyValGlySerGly 62
Db 244 GCGCGGAGAGAGCGCGCGCGCGCGGAGCAACGCGCGCGCGGACAGAGCTCGGG 303
Qy 63 -----HisTrpGluLeuArgCysHisArgLeuGlnAspSerLeuPhe 76
Db 304 CCAAGCGCGCGCGCATCCCGCGCGCGCGCGGTGAGAGAGCTTGGCGGCTGCGGATG 363
Qy 77 SerSerAsp---SerGlyPheSerAspAntyTrArgGlyIleLeuAsnTrp 91
Db 364 CCCGAGACAGAGATGAGCAAAAGCAAGATGCGAGGATTTAGCTCG 411

RESULT 12
US-09-925-065A-490003
; Sequence 490003, Application US/09925065A
```

```
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIORITY FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 490003
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-490003

Alignment Scores:
Pred. No.: 933 Length: 469
Score: 81.00 Matches: 30
Percent Similarity: 39.6% Conservative: 25
Best Local Similarity: 21.6% Mismatches: 49
Query Match: 3.1% Indels: 35
Gaps: 5

US-10-659-800-6 (1-488) x US-09-925-065A-490003 (1-469)
Qy 174 ThrIleLeuCysPheProAlaAlaValAlaLeuLeuValGluSerIleThrProValGly 193
Db 66 AGTGTCTTGTGCTTCTCTCC-----ACCGAATTTT 98
Qy 194 SerLeuLeuAlaLeuMetAlaHisThrIleLeuPheLeuValGluPheSerTrpArgAsp 213
Db 99 GCTCTTCTTCAACGAGAACATATGATGCTTATTCATGAATATTTCTTAATGCTTAA 158
Qy 214 ValAsn-----SerTrpCysArgArgAlaArgAlaValAlaSerAlaGlyValys 231
Db 159 ATMAACTGCAGATGTTGGTGTGGAACACTGAACACATACCTTGAAGCTATCTAATAG 218
Qy 232 AlaSerSerAlaAlaAlaProHisThrValSerTrpProAspAsnLeu---ThrTrpArg 250
Db 219 TTGAATCATAGTATATATATGTCATGTATCTCCCTCAGGTAGTATGATTCAG 278
Qy 251 AspLeuTrpTrpPheLeuPheAlaProThrLeuCysTrpGluLeuAsnPheProArgSer 270
Db 279 GACATTAATAATTTTATTTAT-----TGTACCAAGTTTCTTT----- 317
Qy 271 ProArgIleAlaGlyValArgPheLeuLeuValArgAlaGluMetLeuPheThrGln 290
Db 318 -----ATACTATTCTCTAAT 332
Qy 291 LeuGlnValGlyLeuIle-GlnGlnTrpMetValProThrIleGlnAsnSerMet 308
Db 333 TTGAATGTGATTTTTCACAGATGAGGTTCGCAAGAGTAAAGCAATAGATAG 387

RESULT 13
US-09-925-065A-159096
; Sequence 159096, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
```



```
Db      244 GCTCCGAGAGAGCGCGCGCGCGAGCCARCCGCGCGGCAAGGCTCGGG 303
Qy      63 -----HisTrpGluLeuArgCysHisArgLeuGlnAspSerLeuPhe 76
Db      304 CCAAGCCGGGCGCGCATCCCCGGGCGCCCTGCGCGGTGAAGGCTTGGCGGCTCGGGGTG 363
Qy      77 SerSerAsp---SerGlyPheSerAsnTyrArgGlyIleLeuAsnTrp 91
Db      364 CCGCAGGACAGAGTGGACAAAGCAAGATGGCAGGATCTTAACCTGG 411
```

Search completed: May 7, 2006, 03:12:30
Job time : 653 secs

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GenCore version 5.1.7
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OW protein - protein search, using sw model

Run on: May 5, 2006, 12:44:20 ; Search time 55 Seconds
(without alignments)
3707.286 Million cell updates/sec

Title: US-10-659-800-6
Perfect score: 2594
Sequence: 1 MGDGSSRRRTGSRPSSHG.....VLMYVDYVLYNEAPAAEA 488

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBSCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBSCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2594	100.0	488	US-10-273-438-6	Sequence 6, Appl1
2	2594	100.0	488	US-10-040-315A-6	Sequence 6, Appl1
3	2594	100.0	488	US-10-307-817-544	Sequence 544, App
4	2594	100.0	488	US-10-659-800-6	Sequence 5, Appl1
5	2588	99.8	488	US-11-117-005-5	Sequence 5, Appl1
6	2588	99.8	488	US-10-741-600-1339	Sequence 1339, Ap
7	2588	99.8	488	US-10-741-600-1341	Sequence 1341, Ap
8	2299.5	88.6	500	US-10-157-855-17	Sequence 17, Appl
9	2299.5	88.6	500	US-10-647-517-24	Sequence 24, Appl
10	2292.5	88.4	489	US-10-415-620-2	Sequence 2, Appl1
11	2292.5	88.4	489	US-10-415-620-5	Sequence 5, Appl1
12	2278.5	87.8	498	US-10-482-936-4	Sequence 4, Appl1
13	2278.5	87.8	498	US-11-117-005-4	Sequence 4, Appl1
14	2273.5	87.6	498	US-10-273-438-7	Sequence 7, Appl1
15	2273.5	87.6	498	US-10-273-438-10	Sequence 10, Appl
16	2273.5	87.6	498	US-10-040-315A-7	Sequence 7, Appl1
17	2273.5	87.6	498	US-10-040-315A-10	Sequence 10, Appl
18	2273.5	87.6	498	US-10-659-800-7	Sequence 7, Appl1
19	2273.5	87.6	498	US-10-659-800-10	Sequence 10, Appl
20	2272.5	87.6	498	US-10-482-936-2	Sequence 2, Appl1
21	2264	87.3	497	US-10-690-994-25	Sequence 25, Appl
22	2192.5	84.5	467	US-10-415-620-6	Sequence 6, Appl1
23	2046	78.9	387	US-10-741-600-1340	Sequence 1340, Ap
24	2039	78.6	386	US-10-273-438-5	Sequence 5, Appl1
25	2039	78.6	386	US-10-040-315A-5	Sequence 5, Appl1
26	2039	78.6	386	US-10-659-800-5	Sequence 5, Appl1
27	1681	64.8	421	US-10-741-600-1342	Sequence 1342, Ap

28	1297	50.0	236	US-09-764-853-499	Sequence 499, App
29	1106	42.6	496	US-10-157-855-18	Sequence 18, Appl
30	1106	42.6	496	US-10-369-493-6484	Sequence 6484, Ap
31	1106	42.6	496	US-10-369-493-6485	Sequence 6485, Ap
32	1106	42.6	496	US-10-647-517-14	Sequence 14, Appl
33	840	32.4	517	US-10-424-599-254338	Sequence 254338, A
34	834	32.2	538	US-10-103-247-2	Sequence 49477, A
35	832.5	32.1	501	US-10-103-247-2	Sequence 2, Appl1
36	819	31.6	507	US-10-859-247-19	Sequence 19, Appl
37	819	31.6	507	US-10-859-247-17	Sequence 17, Appl
38	807	31.1	508	US-10-690-994-22	Sequence 22, Appl
39	800.5	30.9	504	US-10-690-994-16	Sequence 16, Appl
40	798.5	30.8	520	US-10-690-994-2	Sequence 2, Appl1
41	797	30.7	532	US-10-223-076-13	Sequence 13, Appl
42	797	30.7	532	US-10-859-247-19	Sequence 19, Appl
43	791.5	30.5	520	US-10-157-855-2	Sequence 2, Appl1
44	791.5	30.5	520	US-10-223-076-3	Sequence 3, Appl1
45	791.5	30.5	520	US-10-690-994-26	Sequence 26, Appl

ALIGNMENTS

```
RESULT 1
US-10-273-438-6
; Sequence 6, Application US/10273438
; Publication No. US200307257A1
; GENERAL INFORMATION:
; APPLICANT: Faese, Robert V.
; APPLICANT: Caese, Sylvaine
; APPLICANT: Smith, Steven
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
; FILE REFERENCE: UCAL-105CIP2
; CURRENT FILING DATE: 2002-10-16
; PRIOR FILING DATE: 2002-10-16
; PRIOR FILING DATE: 2001-10-29
; PRIOR FILING DATE: 2001-10-29
; PRIOR FILING DATE: 1998-11-09
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 488
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-273-438-6

Query Match      100.0%; Score 2594; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 8.9e-23;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MGDGSSRRRTGSRPSSHGCGGPAABEVRDAAAGFDVGAAGDAPAPAPNKGDAVG 60
DB      1 MGDGSSRRRTGSRPSSHGCGGPAABEVRDAAAGFDVGAAGDAPAPAPNKGDAVG 60
QY      61 SGHWEIRCHRIODLFFSSDSGFSNYRGILMVCVMTLISNRLPLENLIKGIIVDP1QV 120
DB      61 SGHWEIRCHRIODLFFSSDSGFSNYRGILMVCVMTLISNRLPLENLIKGIIVDP1QV 120
QY      121 VSLFLKDPHSWPAPCLVIAANVFVAFAFOVEKRLAVGALTQAGILLHVNLAATILCFPA 180
DB      121 VSLFLKDPHSWPAPCLVIAANVFVAFAFOVEKRLAVGALTQAGILLHVNLAATILCFPA 180
QY      181 AVVILVESITPVGSILMAHMTIILFLKLFSTRDVNSWCRARAPAAASAGKKAASSAAAPHT 240
DB      181 AVVILVESITPVGSILMAHMTIILFLKLFSTRDVNSWCRARAPAAASAGKKAASSAAAPHT 240
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QY 241 VSYPDNLTYYRDLYYFLFAPPTLCYELNPPSPRIKRRFLLRRIEMLFPTOLQVGLIQOMM 300
Db 241 VSYPDNLTYYRDLYYFLFAPPTLCYELNPPSPRIKRRFLLRRIEMLFPTOLQVGLIQOMM 300
QY 301 VPTI0NSMKPFKMDYSRIIERLLKLAVPNHLIWLIFYYWLFHSCINAVALMOFGDREF 360
Db 301 VPTI0NSMKPFKMDYSRIIERLLKLAVPNHLIWLIFYYWLFHSCINAVALMOFGDREF 360
QY 361 YRDWNNSESVTYFWQNNNIPVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAFPHXYLVS 420
Db 361 YRDWNNSESVTYFWQNNNIPVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAFPHXYLVS 420
QY 421 VPLRMFRMAFTGMAAOIPLAMFVGRFFQGNYGNAAWLSLIIIGOPIAVLMYVDYYVLN 480
Db 421 VPLRMFRMAFTGMAAOIPLAMFVGRFFQGNYGNAAWLSLIIIGOPIAVLMYVDYYVLN 480
QY 481 YEAPAAEA 488
Db 481 YEAPAAEA 488

RESULT 2
US-10-040-315A-6
; Sequence 6, Application US/10040315A
; Publication No. US20030167483A1
; GENERAL INFORMATION:
; APPLICANT: Fareese, Robert V.
; APPLICANT: Caees, Sylvaine
; APPLICANT: Smith, Steven
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
; FILE REFERENCE: UCAL-105CIP2
; CURRENT APPLICATION NUMBER: US/10/040,315A
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 6
; LENGTH: 488
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-040-315A-6

Query Match 100.0%; Score 2594; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 8.9e-233;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDGSSRRRRRTGSRPSSHGCGGPAALAEVEYRDAAAGPDVGAAGDAPAPAPNKGDDAGVG 60
Db 1 MGDGSSRRRRRTGSRPSSHGCGGPAALAEVEYRDAAAGPDVGAAGDAPAPAPNKGDDAGVG 60
QY 61 SGHWELRCHRLQDSLFSGDSGFSNYRGILNMCVWMLIISNARLFLENLIKYGILVDP1QV 120
Db 61 SGHWELRCHRLQDSLFSGDSGFSNYRGILNMCVWMLIISNARLFLENLIKYGILVDP1QV 120
QY 121 VSLFKDPSHWPAPCLVIAANVFVAAFQVEKRLAVGALTEQAGLLHVANLATILCPFA 180
Db 121 VSLFKDPSHWPAPCLVIAANVFVAAFQVEKRLAVGALTEQAGLLHVANLATILCPFA 180
QY 181 AVVLIVESTITVGSLLAMAHITILFLKLFSTRDVNSWCRBARAKAASAGKASAAAPHT 240
Db 181 AVVLIVESTITVGSLLAMAHITILFLKLFSTRDVNSWCRBARAKAASAGKASAAAPHT 240
QY 241 VSYPDNLTYYRDLYYFLFAPPTLCYELNPPSPRIKRRFLLRRIEMLFPTOLQVGLIQOMM 300
Db 241 VSYPDNLTYYRDLYYFLFAPPTLCYELNPPSPRIKRRFLLRRIEMLFPTOLQVGLIQOMM 300

Db 241 VSYPDNLTYYRDLYYFLFAPPTLCYELNPPSPRIKRRFLLRRIEMLFPTOLQVGLIQOMM 300
QY 301 VPTI0NSMKPFKMDYSRIIERLLKLAVPNHLIWLIFYYWLFHSCINAVALMOFGDREF 360
Db 301 VPTI0NSMKPFKMDYSRIIERLLKLAVPNHLIWLIFYYWLFHSCINAVALMOFGDREF 360
QY 361 YRDWNNSESVTYFWQNNNIPVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAFPHXYLVS 420
Db 361 YRDWNNSESVTYFWQNNNIPVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAFPHXYLVS 420
QY 421 VPLRMFRMAFTGMAAOIPLAMFVGRFFQGNYGNAAWLSLIIIGOPIAVLMYVDYYVLN 480
Db 421 VPLRMFRMAFTGMAAOIPLAMFVGRFFQGNYGNAAWLSLIIIGOPIAVLMYVDYYVLN 480
QY 481 YEAPAAEA 488
Db 481 YEAPAAEA 488

RESULT 3
US-10-307-817-544
; Sequence 544, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agree et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: Curselist version 0.1
; SEQ ID NO: 544
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-544

Query Match 100.0%; Score 2594; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 8.9e-233;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDGSSRRRRRTGSRPSSHGCGGPAALAEVEYRDAAAGPDVGAAGDAPAPAPNKGDDAGVG 60
Db 1 MGDGSSRRRRRTGSRPSSHGCGGPAALAEVEYRDAAAGPDVGAAGDAPAPAPNKGDDAGVG 60
QY 61 SGHWELRCHRLQDSLFSGDSGFSNYRGILNMCVWMLIISNARLFLENLIKYGILVDP1QV 120
Db 61 SGHWELRCHRLQDSLFSGDSGFSNYRGILNMCVWMLIISNARLFLENLIKYGILVDP1QV 120
QY 121 VSLFKDPSHWPAPCLVIAANVFVAAFQVEKRLAVGALTEQAGLLHVANLATILCPFA 180
Db 121 VSLFKDPSHWPAPCLVIAANVFVAAFQVEKRLAVGALTEQAGLLHVANLATILCPFA 180
QY 181 AVVLIVESTITVGSLLAMAHITILFLKLFSTRDVNSWCRBARAKAASAGKASAAAPHT 240
Db 181 AVVLIVESTITVGSLLAMAHITILFLKLFSTRDVNSWCRBARAKAASAGKASAAAPHT 240
QY 241 VSYPDNLTYYRDLYYFLFAPPTLCYELNPPSPRIKRRFLLRRIEMLFPTOLQVGLIQOMM 300
Db 241 VSYPDNLTYYRDLYYFLFAPPTLCYELNPPSPRIKRRFLLRRIEMLFPTOLQVGLIQOMM 300
QY 301 VPTI0NSMKPFKMDYSRIIERLLKLAVPNHLIWLIFYYWLFHSCINAVALMOFGDREF 360
Db 301 VPTI0NSMKPFKMDYSRIIERLLKLAVPNHLIWLIFYYWLFHSCINAVALMOFGDREF 360
QY 361 YRDWNNSESVTYFWQNNNIPVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAFPHXYLVS 420
Db 361 YRDWNNSESVTYFWQNNNIPVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAFPHXYLVS 420
QY 421 VPLRMFRMAFTGMAAOIPLAMFVGRFFQGNYGNAAWLSLIIIGOPIAVLMYVDYYVLN 480
Db 421 VPLRMFRMAFTGMAAOIPLAMFVGRFFQGNYGNAAWLSLIIIGOPIAVLMYVDYYVLN 480

QY 481 YEAPAAEA 488
Db 481 YEAPAAEA 488

RESULT 4
US-10-659-800-6
; Sequence 6, Application US/10659800
; Publication No. US20040078836A1
; GENERAL INFORMATION:
; APPLICANT: Fateese, Robert V.
; APPLICANT: Cases, Sylvaine
; APPLICANT: Smith, Steven
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
; FILE REFERENCE: UCAL-105CIP2CON2
; CURRENT APPLICATION NUMBER: US/10/659,800
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 488
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-659-800-6

Query Match 100.0%; Score 2594; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 8.9e-233;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDGSSRRRTGSRPSSHHGGGPPAAAEVVDAAAGPDVGAAGDAPAPAPKODGAVG 60
Db 1 MGDGSSRRRTGSRPSSHHGGGPPAAAEVVDAAAGPDVGAAGDAPAPAPKODGAVG 60
QY 61 SGHWEIRCHRLQDSLFSDDSGFSNYRGILMNCVWMLISNARLFLENLIKGIIVDP1QV 120
Db 61 SGHWEIRCHRLQDSLFSDDSGFSNYRGILMNCVWMLISNARLFLENLIKGIIVDP1QV 120
QY 121 VSLFKDPSHPAPCLVIAAVFAVAFAVEKRLAVGALTEOAGLLHVNMLATTLCPFA 180
Db 121 VSLFKDPSHPAPCLVIAAVFAVAFAVEKRLAVGALTEOAGLLHVNMLATTLCPFA 180
QY 181 AVVLIVESTIPVGSILMAHTIIFLKLFSYRDVNSWCRARAKAASAGKASSAAABHT 240
Db 181 AVVLIVESTIPVGSILMAHTIIFLKLFSYRDVNSWCRARAKAASAGKASSAAABHT 240
QY 241 VSYPDNLTYYRDLYYFLFAPTLCELNPPRSRIRKRLRRLLEMLFTTOLQVGLIOQM 300
Db 241 VSYPDNLTYYRDLYYFLFAPTLCELNPPRSRIRKRLRRLLEMLFTTOLQVGLIOQM 300
QY 301 VPTI0NSMKPKMDYSRIIRLKLAVPNHLIWLIFPYMLFHSCLNAVAELMOPGDBEF 360
Db 301 VPTI0NSMKPKMDYSRIIRLKLAVPNHLIWLIFPYMLFHSCLNAVAELMOPGDBEF 360
QY 361 YRDWNNSESVTYFMQNNNI PVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAFHEYLVS 420
Db 361 YRDWNNSESVTYFMQNNNI PVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAFHEYLVS 420
QY 421 VPLMFRLMAFTGMAAOIPLAMFVGRFQGNVGNAAVWLSLIGQPIAVLVYVHDYYVLN 480
Db 421 VPLMFRLMAFTGMAAOIPLAMFVGRFQGNVGNAAVWLSLIGQPIAVLVYVHDYYVLN 480
QY 481 YEAPAAEA 488

Db 481 YEAPAAEA 488

RESULT 5
US-11-117-005-5
; Sequence 5, Application US/11117005
; Publication No. US20050193446A1
; GENERAL INFORMATION:
; APPLICANT: Zou, Jitao
; APPLICANT: Taylor, David C
; APPLICANT: Wei, Yangdou
; APPLICANT: Jako, Colette C
; TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
; FILE REFERENCE: 3015-5684.1US
; CURRENT APPLICATION NUMBER: US/11/117,005
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: 09/623,514
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/CA99/01202
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/112,812
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 488
; TYPE: PRT
; ORGANISM: human
US-11-117-005-5

Query Match 100.0%; Score 2594; DB 6; Length 488;
Best Local Similarity 100.0%; Pred. No. 8.9e-233;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDGSSRRRTGSRPSSHHGGGPPAAAEVVDAAAGPDVGAAGDAPAPAPKODGAVG 60
Db 1 MGDGSSRRRTGSRPSSHHGGGPPAAAEVVDAAAGPDVGAAGDAPAPAPKODGAVG 60
QY 61 SGHWEIRCHRLQDSLFSDDSGFSNYRGILMNCVWMLISNARLFLENLIKGIIVDP1QV 120
Db 61 SGHWEIRCHRLQDSLFSDDSGFSNYRGILMNCVWMLISNARLFLENLIKGIIVDP1QV 120
QY 121 VSLFKDPSHPAPCLVIAAVFAVAFAVEKRLAVGALTEOAGLLHVNMLATTLCPFA 180
Db 121 VSLFKDPSHPAPCLVIAAVFAVAFAVEKRLAVGALTEOAGLLHVNMLATTLCPFA 180
QY 181 AVVLIVESTIPVGSILMAHTIIFLKLFSYRDVNSWCRARAKAASAGKASSAAABHT 240
Db 181 AVVLIVESTIPVGSILMAHTIIFLKLFSYRDVNSWCRARAKAASAGKASSAAABHT 240
QY 241 VSYPDNLTYYRDLYYFLFAPTLCELNPPRSRIRKRLRRLLEMLFTTOLQVGLIOQM 300
Db 241 VSYPDNLTYYRDLYYFLFAPTLCELNPPRSRIRKRLRRLLEMLFTTOLQVGLIOQM 300
QY 301 VPTI0NSMKPKMDYSRIIRLKLAVPNHLIWLIFPYMLFHSCLNAVAELMOPGDBEF 360
Db 301 VPTI0NSMKPKMDYSRIIRLKLAVPNHLIWLIFPYMLFHSCLNAVAELMOPGDBEF 360
QY 361 YRDWNNSESVTYFMQNNNI PVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAFHEYLVS 420
Db 361 YRDWNNSESVTYFMQNNNI PVHKWCIRHFYKPMRLRGSSKMMARTGVFLASAFHEYLVS 420
QY 421 VPLMFRLMAFTGMAAOIPLAMFVGRFQGNVGNAAVWLSLIGQPIAVLVYVHDYYVLN 480
Db 421 VPLMFRLMAFTGMAAOIPLAMFVGRFQGNVGNAAVWLSLIGQPIAVLVYVHDYYVLN 480
QY 481 YEAPAAEA 488
Db 481 YEAPAAEA 488

RESULT 6

US-10-741-600-1339
; Sequence 1339, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1339
; LENGTH: 488
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-741-600-1339

Query Match
Best Local Similarity 99.8%; Score 2588; DB 5; Length 488;
Matches 487; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDGSSRRRTGSRPSSHGGGCPAAAEVYRDAAAGPDVGAAGDAPAPAPNKDGDAGVG 60
DB 1 MGDGSSRRRTGSRPSSHGGGCPAAAEVYRDAAAGPDVGAAGDAPAPAPNKDGDAGVG 60
QY 61 SGHWELRCHRLQDSLFSGDSGFSNYRGILNMCVWMLLSNARLFLENLIKXGILVDP1QV 120
DB 61 SGHWELRCHRLQDSLFSGDSGFSNYRGILNMCVWMLLSNARLFLENLIKXGILVDP1QV 120
QY 121 VSLFLKDPHSPAPCLVIAANVFVAFAVEKRLAVGALTQAGLLHVNANLATTLCFPA 180
DB 121 VSLFLKDPHSPAPCLVIAANVFVAFAVEKRLAVGALTQAGLLHVNANLATTLCFPA 180
QY 121 VSLFLKDPHSPAPCLVIAANVFVAFAVEKRLAVGALTQAGLLHVNANLATTLCFPA 180
DB 121 VSLFLKDPHSPAPCLVIAANVFVAFAVEKRLAVGALTQAGLLHVNANLATTLCFPA 180
QY 181 AVVLVSEITPVGSLALMAHTILFLKLFYRDVNSCRPARAKASAGKASSAAAPT 240
DB 181 AVVLVSEITPVGSLALMAHTILFLKLFYRDVNSCRPARAKASAGKASSAAAPT 240
QY 241 VSYPDNLTYRDLVYFLFAPFLCYELNPPRSRIRKRLRILEMFFTOLOVGLIQOM 300
DB 241 VSYPDNLTYRDLVYFLFAPFLCYELNPPRSRIRKRLRILEMFFTOLOVGLIQOM 300
QY 301 VPTIÖNSMKPFKMDYSRIIERLLKLAVPNHLIWLIFYYLPHSCLNAVAELMOFGDREF 360
DB 301 VPTIÖNSMKPFKMDYSRIIERLLKLAVPNHLIWLIFYYLPHSCLNAVAELMOFGDREF 360
QY 361 YRDWNNSESYTYFWQNNIIPVHKICIRHFYKPMLRGSSKMMARTGVFLASAFHEHYLS 420
DB 361 YRDWNNSESYTYFWQNNIIPVHKICIRHFYKPMLRGSSKMMARTGVFLASAFHEHYLS 420
QY 421 VPLMFRLMAFTGMAOIPLAMPVGRFQGNYGNAAVMLSLIIGPIAVLAVYHDYVYLN 480
DB 421 VPLMFRLMAFTGMAOIPLAMPVGRFQGNYGNAAVMLSLIIGPIAVLAVYHDYVYLN 480
QY 481 YEAPAAEA 488
DB 481 YEAPAAEA 488

RESULT 7
US-10-741-600-1341
; Sequence 1341, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1341

LENGTH: 488
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-741-600-1341

Query Match
Best Local Similarity 99.8%; Score 2588; DB 5; Length 488;
Matches 487; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDGSSRRRTGSRPSSHGGGCPAAAEVYRDAAAGPDVGAAGDAPAPAPNKDGDAGVG 60
DB 1 MGDGSSRRRTGSRPSSHGGGCPAAAEVYRDAAAGPDVGAAGDAPAPAPNKDGDAGVG 60
QY 61 SGHWELRCHRLQDSLFSGDSGFSNYRGILNMCVWMLLSNARLFLENLIKXGILVDP1QV 120
DB 61 SGHWELRCHRLQDSLFSGDSGFSNYRGILNMCVWMLLSNARLFLENLIKXGILVDP1QV 120
QY 121 VSLFLKDPHSPAPCLVIAANVFVAFAVEKRLAVGALTQAGLLHVNANLATTLCFPA 180
DB 121 VSLFLKDPHSPAPCLVIAANVFVAFAVEKRLAVGALTQAGLLHVNANLATTLCFPA 180
QY 121 VSLFLKDPHSPAPCLVIAANVFVAFAVEKRLAVGALTQAGLLHVNANLATTLCFPA 180
DB 121 VSLFLKDPHSPAPCLVIAANVFVAFAVEKRLAVGALTQAGLLHVNANLATTLCFPA 180
QY 181 AVVLVSEITPVGSLALMAHTILFLKLFYRDVNSCRPARAKASAGKASSAAAPT 240
DB 181 AVVLVSEITPVGSLALMAHTILFLKLFYRDVNSCRPARAKASAGKASSAAAPT 240
QY 241 VSYPDNLTYRDLVYFLFAPFLCYELNPPRSRIRKRLRILEMFFTOLOVGLIQOM 300
DB 241 VSYPDNLTYRDLVYFLFAPFLCYELNPPRSRIRKRLRILEMFFTOLOVGLIQOM 300
QY 301 VPTIÖNSMKPFKMDYSRIIERLLKLAVPNHLIWLIFYYLPHSCLNAVAELMOFGDREF 360
DB 301 VPTIÖNSMKPFKMDYSRIIERLLKLAVPNHLIWLIFYYLPHSCLNAVAELMOFGDREF 360
QY 361 YRDWNNSESYTYFWQNNIIPVHKICIRHFYKPMLRGSSKMMARTGVFLASAFHEHYLS 420
DB 361 YRDWNNSESYTYFWQNNIIPVHKICIRHFYKPMLRGSSKMMARTGVFLASAFHEHYLS 420
QY 421 VPLMFRLMAFTGMAOIPLAMPVGRFQGNYGNAAVMLSLIIGPIAVLAVYHDYVYLN 480
DB 421 VPLMFRLMAFTGMAOIPLAMPVGRFQGNYGNAAVMLSLIIGPIAVLAVYHDYVYLN 480
QY 481 YEAPAAEA 488
DB 481 YEAPAAEA 488

RESULT 8
US-10-157-855-17
; Sequence 17, Application US/10157855
; Publication No. US20020170091A1
; GENERAL INFORMATION:
; APPLICANT: Lasener, Michael W.
; APPLICANT: Ruzsineky, Diane M.
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; FILE REFERENCE: Acid Sequences
; FILE REFERENCE: 16516.158
; CURRENT APPLICATION NUMBER: US/10/157,855
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 09/326,203
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 500
; TYPE: PR
; ORGANISM: Rattus sp.
US-10-157-855-17

Query Match
Best Local Similarity 88.6%; Score 2299.5; DB 4; Length 500;

Best Local Similarity 85.9%; Pred. No. 2.7e-205;
Matches 427; Conservative 26; Mismatches 31; Indels 13; Gaps 3;

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Qy 1 MGBR---GSSRRRRRGRSSSHGGGPPAAAEVVDAAAGPVGAAAGAPAPAP----- 51
Db 1 MGBRGAAGSSRRRRRGRSSSVISGGSGGPMVDEEVEVDAAAGPDLGAGGAPAPAPAPAH 60
Qy 52 --MKDGDAGVSGHWEIACHRLQDSLFSDDSGFSNYRGILMNCVWMLISNARLFLENLI 109
Db 61 TRDKRQRTSVGSGHWEIACHRLQDSLFSDDSGFSNYRGILMNCVWMLISNARLFLENLI 120
Qy 110 KYGILVDPIDVVSFLKDPHSPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGILLHV 169
Db 121 KYGILVDPIDVVSFLKDPHSPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGILLHV 180
Qy 170 ANLATTICFPAAVVLVESITPVGSLALMAHTILFLKLSFYRDVNSMC--RRAKAKAS 227
Db 181 VNLATTICFPAAVVLVESITPVGSLFALASYSIIFLKLSFYRDVNLWCQRQRRVAKAVS 240
Qy 228 AGKAKASAAAPHTVSYPNLTYYRDLYYFLFAPTLCEYLNFPSPRIIRKFLRLILEMLF 287
Db 241 AGKAVSGAAAGNTVSYPNLTYYRDLYYFLFAPTLCEYLNFPSPRIIRKFLRLILEMLF 300
Qy 288 FTQLQVGLIQOMMVPITONSMKPFKDMYSRIIEBLKLAVPNHLIMLIFFYMLFHSCLN 347
Db 301 FTQLQVGLIQOMMVPITONSMKPFKDMYSRIIEBLKLAVPNHLIMLIFFYMLFHSCLN 360
Qy 348 AVAELMQGDEEFYEDMNNSEVTFWQNNMIPVHKCIRHFYKEMLRGSSKMMARIGV 407
Db 361 AVAELMQGDEEFYEDMNNSEVTFWQNNMIPVHKCIRHFYKEMLRGSSKMMARIGV 420
Qy 408 FLASAFHEIYVSVDLRFRLMAFTGMAQIPLAWFVGRFQNGYGNAAVWLSLIIGQPI 467
Db 421 FLASAFHEIYVSVDLRFRLMAFTGMAQIPLAWFVGRFQNGYGNAAVWLSLIIGQPI 480
Qy 468 AVLMYVHDYVYLVNYPAP 484
Db 481 AVLMYVHDYVYLVNYPAP 497

RESULT 9
US-10-647-517-24
; Sequence 24, Application US/10647517
; Publication No. US20050102716A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROID
; FILE REFERENCE: MTC 6462.1
; CURRENT APPLICATION NUMBER: US/10/647,517
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/548,256
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/1128,995
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 500
; TYPE: PRT
; ORGANISM: rat
US-10-647-517-24
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Query Match 88.6%; Score 2299.5; DB 5; Length 500;

Best Local Similarity 85.9%; Pred. No. 2.7e-205;
Matches 427; Conservative 26; Mismatches 31; Indels 13; Gaps 3;

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Qy 1 MGBR---GSSRRRRRGRSSSHGGGPPAAAEVVDAAAGPVGAAAGAPAPAP----- 51
Db 1 MGBRGAAGSSRRRRRGRSSSVISGGSGGPMVDEEVEVDAAAGPDLGAGGAPAPAPAH 60
Qy 52 --MKDGDAGVSGHWEIACHRLQDSLFSDDSGFSNYRGILMNCVWMLISNARLFLENLI 109
Db 52 --MKDGDAGVSGHWEIACHRLQDSLFSDDSGFSNYRGILMNCVWMLISNARLFLENLI 109
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Db 61 TRDKRQRTSVGSGHWEIACHRLQDSLFSDDSGFSNYRGILMNCVWMLISNARLFLENLI 120
Qy 110 KYGILVDPIDVVSFLKDPHSPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGILLHV 169
Db 121 KYGILVDPIDVVSFLKDPHSPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGILLHV 180
Qy 170 ANLATTICFPAAVVLVESITPVGSLALMAHTILFLKLSFYRDVNSMC--RRAKAKAS 227
Db 181 VNLATTICFPAAVVLVESITPVGSLFALASYSIIFLKLSFYRDVNLWCQRQRRVAKAVS 240
Qy 228 AGKAKASAAAPHTVSYPNLTYYRDLYYFLFAPTLCEYLNFPSPRIIRKFLRLILEMLF 287
Db 241 AGKAVSGAAAGNTVSYPNLTYYRDLYYFLFAPTLCEYLNFPSPRIIRKFLRLILEMLF 300
Qy 288 FTQLQVGLIQOMMVPITONSMKPFKDMYSRIIEBLKLAVPNHLIMLIFFYMLFHSCLN 347
Db 301 FTQLQVGLIQOMMVPITONSMKPFKDMYSRIIEBLKLAVPNHLIMLIFFYMLFHSCLN 360
Qy 348 AVAELMQGDEEFYEDMNNSEVTFWQNNMIPVHKCIRHFYKEMLRGSSKMMARIGV 407
Db 361 AVAELMQGDEEFYEDMNNSEVTFWQNNMIPVHKCIRHFYKEMLRGSSKMMARIGV 420
Qy 408 FLASAFHEIYVSVDLRFRLMAFTGMAQIPLAWFVGRFQNGYGNAAVWLSLIIGQPI 467
Db 421 FLASAFHEIYVSVDLRFRLMAFTGMAQIPLAWFVGRFQNGYGNAAVWLSLIIGQPI 480
Qy 468 AVLMYVHDYVYLVNYPAP 484
Db 481 AVLMYVHDYVYLVNYPAP 497
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RESULT 10

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US-10-415-620-2
; Sequence 2, Application US/10415620
; Publication No. US20040076977A1
; GENERAL INFORMATION:
; APPLICANT: REID, SUZANNE J
; APPLICANT: FORD, CHRISTINE A
; APPLICANT: GEORGES, MICHEL A J
; APPLICANT: COPPIETERS, WOUTER H R
; APPLICANT: GRISART, BERNARD M J J
; APPLICANT: SNEEL, RUSSELL G
; APPLICANT: SPELMAN, RICHARD J
; TITLE OF INVENTION: MARKER ASSISTED SELECTION OF BOVINE FOR IMPROVED MILK COMPOSITION
; FILE REFERENCE: P452508 CIE
; CURRENT APPLICATION NUMBER: US/10/415,620
; CURRENT FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9434)..(9434)
; OTHER INFORMATION: ambiguous nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9436)..(9496)
; OTHER INFORMATION: ambiguous nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10402)..(10417)
; OTHER INFORMATION: ambiguous nucleotides
US-10-415-620-2
```

Query Match 88.4%; Score 2292.5; DB 4; Length 489;
Best Local Similarity 88.0%; Pred. No. 1.2e-204;

Matches 434; Conservative 15; Mismatches 31; Indels 13; Gaps 3;

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OY 1 MGDR---GSSRRRTGSRPSHGGCGPAAAEVVDAAAGPVGAGAPAPAPBNKGDGA 57
D 1 MGDGAGAGSGRRRTGSRPSIQGSGGPAAAEVVR-----DVAGGDAAPRDTDKGDV 54
OY 58 GVGSGHWEIARHRLQDSLFSSDSGFSNRYGILNMCVWMLISNARLPLENLIKGIIVDP 117
D 55 DVGSGHMLRCHRLQDSLFSDDSGFSNRYGILNMCVWMLISNARLPLENLIKGIIVDP 114
OY 118 IQVNSLFKDPHSPAPCLTVIAANFAVAAPQVEKRLAVGALTBOAGLLHVANLATTIC 177
D 115 IQVNSLFKDPHSPAPCLTVIAANFAVAAPQVEKRLAVGALTBOAGLLHVANLATTIC 174
OY 178 FPAAVVLVESITPVGSLALMAHTIIFLKLFSYRDVNSMCR---ARAKASAGKAS 233
D 175 FPAAVFLBESITPVGSLALMAHTIIFLKLFSYRDVNSMCRERAGAKAALAGKAN 234
OY 234 SAAPHVTSYPDNLTYRDLYFLFAPTLCELNPPSRIRKRFLRLRILEMFLTQLOV 293
D 235 GGAARVTSYPDNLTYRDLYFLFAPTLCELNPPSRIRKRFLRLRILEMFLTQLOV 294
OY 294 GLIQMWVPTTONSMKPEKMDYSRIERLKLAVPNHLIWFYWLPHSCLNAVAELM 353
D 295 GLIQMWVPAIIONSMKPEKMDYSRIERLKLAVPNHLIWFYWLPHSCLNAVAELM 354
OY 354 QGDRFEFRDMWNSSTYTFQNMNIPVHKCIRHFYKPMRLRSGSSKMAARTAVFLASAF 413
D 355 QGDRFEFRDMWNSSTYTFQNMNIPVHKCIRHFYKPMRLRSGSSKMAARTAVFLASAF 414
OY 414 FHEVLSVPLMFRLMAFTGMAOIPLAVFGRFQNGYGAAYVLSLIGOPTAVLMYV 473
D 415 FHEVLSVPLMFRLMAFTGMAOIPLAVFGRFQNGYGAAYVLSLIGOPTAVLMYV 474
OY 474 HDYVLYNREAPAA 486
D 475 HDYVLYNREAPAA 487
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RESULT 11

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US-10-415-620-5
; Sequence 5, Application US/10415620
; Publication No. US20040076977A1
; GENERAL INFORMATION:
; APPLICANT: REID, SUZANNE J
; APPLICANT: FORD, CHRISTINE A
; APPLICANT: GEORGES, MICHEL A J
; APPLICANT: COPIETERS, WOUTER H R
; APPLICANT: GRISART, BERNARD M J J
; APPLICANT: SNEEL, RUSSELL G
; APPLICANT: SPELMAN, RICHARD J
; TITLE OF INVENTION: MARKER ASSISTED SELECTION OF BOVINE FOR IMPROVED MILK COMPOSITION
; FILE REFERENCE: P452508 CJE
; CURRENT APPLICATION NUMBER: US/10/415,620
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Bos taurus
; NAME/KEY: VARIANT
; LOCATION: (232)..(232)
; OTHER INFORMATION: an amino acid substitution (K -> A) caused by a polymorphism at b
; OTHER INFORMATION: aas 7224-7225 of the genomic sequence (measured from the adenine
; OTHER INFORMATION: residue of the translation start codon). Lysine (K) corresponds
; OTHER INFORMATION: to the Q allele, alanine (A) corresponds to the q allele.
US-10-415-620-5
```

Query Match 88.4%; Score 2292.5; DB 4; Length 489;
Best Local Similarity 88.0%; Pred. No. 1.2e-204;
Matches 434; Conservative 15; Mismatches 31; Indels 13; Gaps 3;

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OY 1 MGDR---GSSRRRTGSRPSHGGCGPAAAEVVDAAAGPVGAGAPAPAPBNKGDGA 57
D 1 MGDGAGAGSGRRRTGSRPSIQGSGGPAAAEVVR-----DVAGGDAAPRDTDKGDV 54
OY 58 GVGSGHWEIARHRLQDSLFSSDSGFSNRYGILNMCVWMLISNARLPLENLIKGIIVDP 117
D 55 DVGSGHMLRCHRLQDSLFSDDSGFSNRYGILNMCVWMLISNARLPLENLIKGIIVDP 114
OY 118 IQVNSLFKDPHSPAPCLTVIAANFAVAAPQVEKRLAVGALTBOAGLLHVANLATTIC 177
D 115 IQVNSLFKDPHSPAPCLTVIAANFAVAAPQVEKRLAVGALTBOAGLLHVANLATTIC 174
OY 178 FPAAVVLVESITPVGSLALMAHTIIFLKLFSYRDVNSMCR---ARAKASAGKAS 233
D 175 FPAAVFLBESITPVGSLALMAHTIIFLKLFSYRDVNSMCRERAGAKAALAGKAN 234
OY 234 SAAPHVTSYPDNLTYRDLYFLFAPTLCELNPPSRIRKRFLRLRILEMFLTQLOV 293
D 235 GGAARVTSYPDNLTYRDLYFLFAPTLCELNPPSRIRKRFLRLRILEMFLTQLOV 294
OY 294 GLIQMWVPTTONSMKPEKMDYSRIERLKLAVPNHLIWFYWLPHSCLNAVAELM 353
D 295 GLIQMWVPAIIONSMKPEKMDYSRIERLKLAVPNHLIWFYWLPHSCLNAVAELM 354
OY 354 QGDRFEFRDMWNSSTYTFQNMNIPVHKCIRHFYKPMRLRSGSSKMAARTAVFLASAF 413
D 355 QGDRFEFRDMWNSSTYTFQNMNIPVHKCIRHFYKPMRLRSGSSKMAARTAVFLASAF 414
OY 414 FHEVLSVPLMFRLMAFTGMAOIPLAVFGRFQNGYGAAYVLSLIGOPTAVLMYV 473
D 415 FHEVLSVPLMFRLMAFTGMAOIPLAVFGRFQNGYGAAYVLSLIGOPTAVLMYV 474
OY 474 HDYVLYNREAPAA 486
D 475 HDYVLYNREAPAA 487
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RESULT 12

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US-10-482-936-4
; Sequence 4, Application US/10482936
; Publication No. US20040234986A1
; GENERAL INFORMATION:
; APPLICANT: Arbeitsgemeinschaft Deutscher Rindzochter e.V.
; TITLE OF INVENTION: Method of testing a mammal for its predisposition for
; TITLE OF INVENTION: fat content of milk and/or its predisposition for meat
; TITLE OF INVENTION: mapping
; FILE REFERENCE: F 1078 EP
; CURRENT APPLICATION NUMBER: US/10/482,936
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-482-936-4
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Query Match 87.8%; Score 2278.5; DB 5; Length 489;
Best Local Similarity 87.8%; Pred. No. 2.3e-203; Indels 13; Gaps 3;
Matches 433; Conservative 14; Mismatches 33;
OY 1 MGDR---GSSRRRTGSRPSHGGCGPAAAEVVDAAAGPVGAGAPAPAPBNKGDGA 57
D 1 MGDGAGAGSGRRRTGSRPSIQGSGGPAAAEVVR-----DVAGGDAAPRDTDKGDV 54
OY 58 GVGSGHWEIARHRLQDSLFSSDSGFSNRYGILNMCVWMLISNARLPLENLIKGIIVDP 117
D 55 DVGSGHMLRCHRLQDSLFSDDSGFSNRYGILNMCVWMLISNARLPLENLIKGIIVDP 114
OY 118 IQVNSLFKDPHSPAPCLTVIAANFAVAAPQVEKRLAVGALTBOAGLLHVANLATTIC 177
D 115 IQVNSLFKDPHSPAPCLTVIAANFAVAAPQVEKRLAVGALTBOAGLLHVANLATTIC 174


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Db 241 KKVSGAAAOQAVSYPDNLTYRDLYYFIAPFLCYELNPPRSPIRKQFLLRRLVLEMLFFT 300
Qy 290 QLOVGLIQOMWVPTIQNSMKPFKMDYSRIIERLLKLAVPNHLIWLIFPYLPHSCINAV 349
Db 301 QLOVGLIQOMWVPTIHSNMPKFKMDYSRIIERLLKLAVPNHLIWLIFPYLPHSCINAV 360
Qy 350 AELMQGDFREFYRDWMSSEVTYFWQNNIPVHKCIRHFYKPMRLRGSSKMMARTGVFL 409
Db 361 AELMQGDFREFYRDWMSSEVTYFWQNNIPVHKCIRHFYKPMRLRGSSKMMARTGVFL 420
Qy 410 ASAFHEHYLVSVPLRMFLMAFTGMAQIPLAMFVGRFFQGNYGNAAVWLSLIIGQPIAV 469
Db 421 TSAFFHEHYLVSVPLRMFLMAFTAMMAQVPLAMIVGRFFQGNYGNAAVWVTLIIGQPIAV 480
Qy 470 LMYVHDYVLYNLYEAP 484
Db 481 LMYVHDYVLYNLYDAP 495
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RESULT 15
US-10-273-438-10
/ Sequence 10, Application US/10273438
/ Publication NO. US20030072157A1
/ GENERAL INFORMATION:
/ APPLICANT: Farese, Robert V.
/ APPLICANT: Cages, Sylvaine
/ APPLICANT: Smith, Steven
/ APPLICANT: Erickson, Sandra
/ TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
/ FILE REFERENCE: UCAL-105CIP2
/ CURRENT APPLICATION NUMBER: US/10/273,438
/ PRIOR FILING DATE: 2002-10-16
/ PRIOR APPLICATION NUMBER: US/10/040,315
/ PRIOR FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: 60/107,771
/ PRIOR FILING DATE: 1998-11-09
/ PRIOR APPLICATION NUMBER: PCT/US98/17883
/ PRIOR FILING DATE: 1998-08-28
/ PRIOR APPLICATION NUMBER: 09/103,754
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 09/339,472
/ PRIOR FILING DATE: 1999-06-23
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 10
/ LENGTH: 498
/ TYPE: PRT
/ ORGANISM: mus musculus
US-10-273-438-10
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Query Match 87.6%; Score 2273.5; DB 4; Length 498;
Beet Local Similarity 84.8%; Pred. No. 7e-203;
Matches 420; Conservative 29; Mismatches 35; Indels 11; Gaps 3;
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Qy 1 MGDR---GSSRRRTGSRPSSHGSGGPAABEEVDAAAGPDVGAADAPAPAP----- 51
Db 1 MGDRGGAGSSRRRRGSRVSVQSGSPVKEDEVDAAVSPDLAGADAPAPAPAPAHTR 60
Qy 52 NKDDAGVSGHWEIQRLODSLFSDSGFSNRYGILNMCVMIISNARILENLIXY 111
Db 61 DKDRTSVGDYMDLRCHRLDSLFSDSGFSNRYGILNMCVMIISNARILENLIXY 120
Qy 112 GILVDPIDQVSLFLKDPHSWAPCLVIANVPAVAAPOVEKRLAVALTEQAGILLHYAN 171
Db 121 GILVDPIDQVSLFLKDPYSWAPCVIIASNIIVVAQIEKRLAVALTEQAGILLHYAN 180
Qy 172 LATIICPPAAVVLVVESTIPVGSLLALMAHTLFLKLSYRDVNSMC--RRARAKAASAG 229
Db 181 LATIICPPAAVALVESTIPVGSVALASYSIMFLKLSYRDVNLMCGRKAKAASVSTG 240
Qy 230 KKASSAAAPHTVSYPDNLTYRDLYYFLAPFLCYELNPPRSPIRKQFLLRRLVLEMLFFT 289
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Db 241 KKVSGAAAOQAVSYPDNLTYRDLYYFIAPFLCYELNPPRSPIRKQFLLRRLVLEMLFFT 300
Qy 290 QLOVGLIQOMWVPTIQNSMKPFKMDYSRIIERLLKLAVPNHLIWLIFPYLPHSCINAV 349
Db 301 QLOVGLIQOMWVPTIHSNMPKFKMDYSRIIERLLKLAVPNHLIWLIFPYLPHSCINAV 360
Qy 350 AELMQGDFREFYRDWMSSEVTYFWQNNIPVHKCIRHFYKPMRLRGSSKMMARTGVFL 409
Db 361 AELMQGDFREFYRDWMSSEVTYFWQNNIPVHKCIRHFYKPMRLRGSSKMMARTGVFL 420
Qy 410 ASAFHEHYLVSVPLRMFLMAFTGMAQIPLAMFVGRFFQGNYGNAAVWLSLIIGQPIAV 469
Db 421 TSAFFHEHYLVSVPLRMFLMAFTAMMAQVPLAMIVGRFFQGNYGNAAVWVTLIIGQPIAV 480
Qy 470 LMYVHDYVLYNLYEAP 484
Db 481 LMYVHDYVLYNLYDAP 495
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Search completed: May 5, 2006, 12:46:31
Job time : 57 secs
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